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OW protein - protein search, using sw model

Run on:      June 15, 2004, 12:22:52 ; Search time 55 Seconds
              (without alignments)
              35.961 Million cell updates/sec

Title:        US-09-394-019C-212
Perfect score: 39
Sequence:     1 LEHDGIN 7

Scoring table:  BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:     1566107 seqs, 282547505 residues

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SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	39	100.0	7	4	ABG73286
2	39	100.0	7	5	ABU60442
3	39	100.0	18	4	ABG73286
4	39	100.0	18	4	ABG73286
5	35	89.7	7	4	ABG73288
6	35	89.7	7	5	ABU60444
7	35	89.7	18	4	ABG73232
8	35	89.7	18	4	ABG73326
9	34	87.2	18	5	ABP01506
10	34	87.2	124	4	AAU53518
11	34	87.2	124	6	ABM50037
12	31	79.5	30	2	AAV39352
13	30	76.9	7	3	ABB27270
14	30	76.9	7	4	ABG73290
15	30	76.9	7	5	ABU60446
16	30	76.9	18	4	ABG73328
17	30	76.9	18	4	ABG73234
18	29	74.4	5	2	AAV15690
19	29	74.4	7	4	ABG73287
20	29	74.4	7	5	ABU60443
21	29	74.4	18	4	ABG73231
22	29	74.4	18	4	ABG73325
23	29	74.4	20	5	ABB89029
24	29	74.4	20	7	ADE06161
25	29	74.4	38	3	AAAG07964

Query Match 100.0%; Score 39; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
| | | | |
Db 1 LEHGDGIN 7

RESULT 2
ID ABU60442
XX ABU60442 standard; peptide; 7 AA.
AC ABU60442;
XX 29-APR-2003 (first entry)
DT Protease binding peptide motif SEQ ID 166.
DE
XX
KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW nuclease; screening; fluorophore; substrate cleavage.
XX
OS Synthetic.
XX WO200261038-A2.
PN
XX
PD 08-AUG-2002.
XX
XX
PF 21-DEC-2001; 2001WO-US049781.
XX
PR 22-DEC-2000; 2000US-00747287.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Packard BS, Komoriya A;
XX
XX WPI; 2002-698548/75.
DR
XX
XX
PT Indicator composition comprising polypeptide or nucleic acid backbone
PT joining two same chromophores resulting in quenching of fluorescence
PT of change in absorbance of chromophores, useful for detecting protease
PT activity.
XX
PS Disclosure; Page 35; 97pp; English.

This invention describes a novel indicator composition (referred as homo-
CC doubly labeled compositions) comprising a polypeptide backbone or a
CC nucleic acid backbone joining two chromophores of the same species
CC whereby the chromophores form an H-dimer resulting in quenching of the
CC fluorescence of or a change in the absorbance of the chromophore, a
CC decrease in fluorescence or a change in absorbance indicates that the
CC first molecule and the second molecule are interacting. The indicator is
CC useful for detecting the activity of a protease, where an increase in
CC fluorescence or a change in absorbance indicates that the protease
CC cleaves the polypeptide backbone. The indicator is attached to a solid
CC support inside a mammalian, yeast or insect cell. The composition bears a
CC hydrophobic group such as Fmoc, 9-fluorenylmethyl group, 1-
CC fluoronaphthyl group, 9-fluorenylmethyl group, and 9-fluorenylmethyl-
CC carboxylic group, benzylloxycarbonyl, Xanthyl (Xan), Trityl (Ttt), 4-
CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3,6-trimethyl-
CC benzenehexyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
CC dimethoxybenzyl (Mdb), etc. The method described in the invention is
CC useful for detecting protease or nuclease activity (or the presence of
CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
CC cultured adherent cells), a biological sample such as tissue, biopsy,
CC lymph, embryo, or whole animal, or cell suspension derived from a
CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
CC The indicator composition is also useful for screening a test agent for
CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
CC indicator reagents allow rapid determination of protease activity in a
CC matter of minutes in a single-step procedure. The fluorescent indicators
CC both absorb and emit in the visible range (400-800 nm). These signals are
CC therefore not readily quenched by, nor is activation of the fluorophores,

that is, absorption of light, interfered with by background molecules;
therefore they are easily detected in biological samples. The fluorogenic
protease indicators utilize high efficiency fluorophores and are able to
achieve a high degree of quenching while providing a strong signal when
the quench is released by cleavage of the peptide substrate. The high
signal allows detection of very low levels of protease activity. Thus the
fluorogenic protease indicators are particularly well suited for in situ
detection of protease activity. ABU60357-ABU60477 represent peptides use
to illustrate the method described in the disclosure of the invention

Sequence 7 AA;
Query Match 100.0%; Score 39; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
| | | | |
Db 1 LEHGDGIN 7

RESULT 3
AAG73324
ID AAG73324 standard; peptide; 18 AA.
XX
AC AAG73324;
XX
XX 14-AUG-2001 (first entry)
DT
XX
DE Protease indicator compound peptide #53.
XX
KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
XX
FH Key
FT Modified-site 4
FT /label= OTHER
FT /note= "designated J in the specification"
FT Modified-site 14
FT /label= OTHER
FT /note= "designated J in the specification"
XX
XX WO200118238-A1.
XX
XX 15-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-US024882.
XX
XX 10-SEP-1999; 99US-00394019.
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Komoriya A, Packard BS;
XX WPI; 2001-389573/41.
XX
XX New fluorogenic compositions whose fluorescence level increases in the
XX presence of active proteases, useful for detecting and localizing
XX protease activity in biological samples, particularly in frozen tissue
XX samples.
XX
XX Claim 4; Page 71; 86pp; English.

The present invention describes fluorogenic compositions which can be
used for the detection of protease activity. This can be useful as an
indicator of viral infection, cancer metastasis, haemophilia, emphysema,
thrombosis and arthritis. The fluorogenic compositions comprise a
peptide, a peptide spacer and a donor and an acceptor fluorophore. The
peptide is cleaved by a protease and the fluorophores can then be
detected. The present sequence is one of the peptides described in the

CC exemplification of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 39; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHGDGIN 7
Db 6 LEHGDGIN 12

RESULT 4
AAG73230
ID AAG73230 standard; peptide; 18 AA.
XX
AC AAG73230;
XX
DT 14-AUG-2001 (first entry)
XX
DE Protease binding site #164.
XX
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "modified by fluorophore"
XX
PN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-US024892.
XX
PR 10-SEP-1999; 99US-00394019.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 2001-389573/41.
XX
PS New fluorogenic compositions whose fluorescence level increases in the
XX presence of active proteases, useful for detecting and localizing
XX protease activity in biological samples, particularly in frozen tissue
XX samples.
XX
SQ Disclosure; Page 29; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 39; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHGDGIN 7
Db 6 LEHGDGIN 12

RESULT 5
AAG73288
ID AAG73288 standard; peptide; 7 AA.
XX
AC AAG73288;
XX
DT 14-AUG-2001 (first entry)
XX
DE Protease indicator compound peptide #17.
XX
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
PN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-US024892.
XX
PR 10-SEP-1999; 99US-00394019.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 2001-389573/41.
XX
PS New fluorogenic compositions whose fluorescence level increases in the
XX presence of active proteases, useful for detecting and localizing
XX protease activity in biological samples, particularly in frozen tissue
XX samples.
XX
SQ Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 7 AA;

Query Match 89.7%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 2 EHDGIN 7

RESULT 6
ABU60444
ID ABU60444 standard; peptide; 7 AA.
XX
AC ABU60444;
XX
DT 29-APR-2003 (first entry)
XX
DE Protease binding peptide motif SEQ ID 168.
XX
XX Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW nuclease; screening; fluorophore; substrate cleavage.
XX
OS Synthetic.

XX FN WO200261038-A2.
 XX PD 08-AUG-2002.
 XX PF 21-DEC-2001; 2001WO-US049781.
 XX PR 22-DEC-2000; 2000US-00747287.
 XX PA (ONCO-) ONCOIMMUNIN INC.
 XX PI Packard BS, Komoriya A;
 XX DR WPI; 2002-698548/75.
 XX FT Indicator composition comprising polypeptide or nucleic acid backbone
 XX PT joining two same chromophores resulting in quenching of fluorescence
 XX FT of/change in absorbance of chromophores, useful for detecting protease
 XX PT activity.
 XX PS Disclosure; Page 35; 97pp; English.
 XX CC This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzeneulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. AB060357-AB060477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention

ID AAG73232 standard; peptide; 18 AA.
 XX AC AAG73232;
 XX DT 14-AUG-2001 (first entry)
 XX DE Protease binding site #166.
 XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "modified by fluorophore"
 XX PN WO200118238-A1.
 XX PD 15-MAR-2001.
 XX PF 11-SEP-2000; 2000WO-US024882.
 XX PR 10-SEP-1999; 99US-00394019.
 XX PA (ONCO-) ONCOIMMUNIN INC.
 XX PI Komoriya A, Packard BS;
 XX DR WPI; 2001-389573/41.
 XX PT New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.
 XX PS Disclosure; Page 29; 86pp; English.
 XX CC The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention
 XX SQ Sequence 18 AA;
 Query Match 89.7%; Score 35; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGIN 7
 Db 7 EHDGIN 12
 RESULT 8
 AAG73326
 ID AAG73326 standard; peptide; 18 AA.
 XX AC AAG73326;
 XX DT 14-AUG-2001 (first entry)
 XX DE Protease indicator compound peptide #55.
 XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.

XX OS Synthetic.
 XX FH Key
 XX FT Location/Qualifiers
 XX FT 4
 XX FT /label= OTHER
 XX FT /note= "designated J in the specification"
 XX FT 14
 XX FT /label= OTHER
 XX FT /note= "designated J in the specification"
 XX FT
 XX PN WO200118238-A1.
 XX PN
 XX PD 15-MAR-2001.
 XX PD
 XX PF 11-SEP-2000; 2000WO-US024882.
 XX PF
 XX PR 10-SEP-1999; 99US-00394019.
 XX PR
 XX PA (ONCO-) ONCOIMMUNIN INC.
 XX PA
 XX PI Komoriya A, Packard BS;
 XX PI
 XX DR WPI; 2001-389573/41.
 XX DR
 XX PT New fluorogenic compositions whose fluorescence level increases in the
 XX PT presence of active proteases, useful for detecting and localizing
 XX PT protease activity in biological samples, particularly in frozen tissue
 XX PT samples.
 XX PS
 XX PS Claim 4; Page 71; 86pp; English.
 XX PS
 XX CC The present invention describes fluorogenic compositions which can be
 XX CC used for the detection of protease activity. This can be useful as an
 XX CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 XX CC thrombosis and arthritis. The fluorogenic compositions comprise a
 XX CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 XX CC peptide is cleaved by a protease and the fluorophores can then be
 XX CC detected. The present sequence is one of the peptides described in the
 XX CC exemplification of the invention
 XX CC
 XX SQ Sequence 18 AA;
 XX SQ
 Query Match 89.7%; Score 35; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGIN 7
 Db 7 EHDGIN 12
 RESULT 9
 ABP01506
 ID ABP01506 standard; protein; 58 AA.
 XX AC ABP01506;
 XX AC
 XX DT 24-JUN-2002 (first entry)
 XX DT
 XX DE Human ORFX protein sequence SEQ ID NO:2994.
 XX DE
 XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 XX KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 XX KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 XX KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 XX KW hypertension; hypothyroidism; cholesterol ester storage disease;
 XX KW immune deficiency; immune disorder; infectious disease;
 XX KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 XX KW myasthenia gravis.
 XX KW
 XX OS Homo sapiens.
 XX OS

PN WO200192523-A2.
 XX PD 06-DEC-2001.
 XX PD
 XX PF 29-MAY-2001; 2001WO-US010836.
 XX PF
 XX PR 30-MAY-2000; 2000US-0206132P.
 XX PR 29-AUG-2000; 2000US-0228716P.
 XX PR
 XX PA (CURA-) CURAGEN CORP.
 XX PA
 XX PI Shimkets RA, Leach MD;
 XX PI
 XX DR WPI; 2002-106308/14.
 XX DR N-PSDB; ABN17258.
 XX DR
 XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
 XX PT preventing and treating cardiovascular disease, neurodegenerative,
 XX PT hyperproliferative disorders and autoimmune disorders.
 XX PT
 XX PS Disclosure; SEQ ID NO 2994; 1037pp; English.
 XX PS
 XX CC The present invention describes substantially purified human proteins
 XX CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 XX CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 XX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 XX CC treating or preventing a pathology associated with an ORFX-associated
 XX CC disorder in humans, and in the manufacture of a medicament for treating a
 XX CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 XX CC sequences can be used in gene therapy. ORFX sequences can be used in the
 XX CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 XX CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 XX CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 XX CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 XX CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 XX CC storage disease, various immune deficiencies and disorders, infectious
 XX CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 XX CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 XX CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 XX CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 XX CC bone degenerative disorders, or periodontal disease, and for gut
 XX CC protection or regeneration and treatment of lung or liver fibrosis,
 XX CC reperfusion injury in various tissues and conditions resulting from
 XX CC systemic cytokine damage. N.B. The sequence data for this patent did not
 XX CC form part of the printed specification, but was obtained in electronic
 XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX CC
 XX SQ Sequence 58 AA;
 XX SQ
 Query Match 87.3%; Score 34; DB 5; Length 58;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEHDGIN 7
 Db 16 LEHDGIS 22
 RESULT 10
 AAU53518
 ID AAU53518 standard; protein; 124 AA.
 XX AC AAU53518;
 XX AC
 XX DT 27-FEB-2002 (first entry)
 XX DT
 XX DE Propionibacterium acnes immunogenic protein #14414.
 XX DE
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX KW dermatological; osteopathic; neuroprotectant.
 XX KW

OS Propionibacterium acnes.
XX WO200181581-A2.
XX 01-NOV-2001.
XX 20-APR-2001; 2001WO-US012865.
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX (CORI-) CORIXA CORP.
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59560.
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX Example 1; SEQ ID NO 14713; 1069pp; English.
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 124 AA;
Query Match 87.2%; Score 34; DB 4; Length 124;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEHDGIN 7
Db 34 LEHDGIS 40
RESULT 11
ABM50037
ID ABM50037 standard; protein; 124 AA.
XX ABM50037;
XX 20-OCT-2003 (first entry)
XX Propionibacterium acnes predicted ORF-encoded polypeptide #14713.
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX Propionibacterium acnes.

PN WO2003033515-A1.
XX 24-APR-2003.
XX 11-OCT-2002; 2002WO-US032727.
XX 15-OCT-2001; 2001US-00978825.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieue-Douglas J;
XX WPI; 2003-381789/36.
XX N-PSDB; ACF64489.
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX Example 1; SEQ ID NO 14713; 1481pp; English.
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 124 AA;
Query Match 87.2%; Score 34; DB 6; Length 124;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEHDGIN 7
Db 34 LEHDGIS 40
RESULT 12
AAV39352
ID AAV39352 standard; peptide; 30 AA.
XX AAV39352;
XX AAV39352;
XX 13-DEC-1999 (first entry)
XX Linker peptide consisting of six tetrapeptide caspase target sites.
XX Fusion protein; repressor; linker; reporter; protease; cleavage site;
KW

KW caspase; linker peptide; caspase; tetrapeptide; target site.
OS Synthetic.
PN WO9947640-A1.
PD 23-SEP-1999.
XX 19-MAR-1999; 99WO-US006070.
PF 20-MAR-1998; 98US-0078721P.
PR 17-MAR-1999; 99US-00270983.
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
PA Hay BA, Hawkins CV;
XX WPI; 1999-571832/48.
DR A protease-dependent reporter fusion protein construct useful in assays
XX to identify proteases.
PS Example 1; Page 34; 64pp; English.
XX This sequence is a linker peptide consisting of six tetrapeptide caspase
CC target sites, each of which is followed by a glycine residue. The glycine
CC residues act as stabilising residues in the N-end rule degradation
CC pathway in yeast. This linker sequence is an essential part of the fusion
CC protein of the invention. The invention relates to a protease-dependent
CC reporter-repressor fusion protein, where protease cleavage increases the
CC activity of the reporter. The fusion protein consists of a reporter
CC polypeptide linked to a linker polypeptide which is linked to a repressor
CC polypeptide. The linker polypeptide contains a protease cleavage site.
CC The repressor polypeptide represses the activity of the reporter
CC polypeptide and is operably linked to the linker polypeptide. Cleavage of
CC the linker polypeptide at the protease cleavage site increases the
CC activity of the reporter. The fusion proteins are useful in assays to
CC identify proteases that recognise specific protease cleavage sites or to
CC identify protease inhibitors or activators. The fusion proteins can be
CC used as reporters e.g. caspase activity molecules that function in living
XX cells
XX Sequence 30 AA;
SQ Query Match 79.5%; Score 31; DB 2; Length 30;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEHGGI 6
DB 11 IEHDGI 16
RESULT 13
AAB27270
ID AAB27270 standard; peptide; 7 AA.
XX AC AAB27270;
XX DT 23-FEB-2001 (first entry)
XX DE Murine CRAM-1 tyrosine kinase phosphorylation signature #2.
XX Immunoglobulin superfamily; Ig Sf; C2 domain; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; mouse;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX OS Mus sp.
XX FN WO200053749-A2.
XX PD 14-SEP-2000.
XX

PF 13-MAR-2000; 2000WO-EP002219.
XX 11-MAR-1999; 99EP-00200746.
XX (RMFD-) RMF DICTAGENE SA.
XX Imhof BA, Aurrand-Lions M;
XX WPI; 2000-587436/55.
DR Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
XX CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX Example; Page 23; 59pp; English.
XX The present sequence comprises one of the two tyrosine kinase
CC phosphorylation signatures found in the murine confluency regulated
CC adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is a member of
CC the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding
CC sequence can be used in the treatment of cancer, inflammation, to
CC modulate cell-cell interactions and angiogenesis, and in the modulation
CC of wound healing
XX Sequence 7 AA;
SQ Query Match 76.9%; Score 30; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGIN 7
DB 1 KHDGVN 6
RESULT 14
AAG73290
ID AAG73290 standard; peptide; 7 AA.
XX AC AAG73290;
XX DT 14-AUG-2001 (first entry)
XX DE Protease indicator compound peptide #19.
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX OS Synthetic.
XX PN WO200118238-A1.
XX PD 15-MAR-2001.
XX PF 11-SEP-2000; 2000WO-US024882.
XX PR 10-SEP-1999; 99US-00394019.
XX PA (ONCO-) ONCOIMMUNIN INC.
XX Komoriya A, Packard BS;
XX WPI; 2001-389573/41.
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
XX samples.
XX Claim 1; Page 70; 86pp; English.
XX The present invention describes fluorogenic compositions which can be

CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 76.9%; Score 30; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDGIN 7
 Db 3 HDGIN 7
 |||||
 |||||
 RESULT 15
 ABU60446
 ID ABU60446 standard; peptide; 7 AA.
 XX
 AC ABU60446;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Protease binding peptide motif SEQ ID 170.
 XX
 KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX
 OS Synthetic.
 XX
 PN WQ200261038-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001WO-US049781.
 XX
 PR 22-DEC-2000; 2000US-00747287.
 XX
 PA (ONCO-) ONCOIMMUNIN INC.
 XX
 PI Packard BS, Komoriya A;
 XX
 XX WPI; 2002-698548/75.
 XX
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 PS Disclosure; Page 35; 97pp; English.
 XX
 CC This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluorenylmethyl group,¹
 CC fluorenylmethyl group, 9-fluorenylmethyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of

CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 76.9%; Score 30; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDGIN 7
 Db 3 HDGIN 7
 |||||
 |||||

RESULT 16
 AAG73328
 ID AAG73328 standard; peptide; 18 AA.
 XX
 AC AAG73328;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Protease indicator compound peptide #57.
 XX
 KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= OTHER
 FT /note= "designated J in the specification"
 FT Modified-site 14 /label= OTHER
 FT /note= "designated J in the specification"
 XX
 PN WO200118238-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-US024882.
 XX
 PR 10-SEP-1999; 99US-00394019.
 XX
 PA (ONCO-) ONCOIMMUNIN INC.
 XX
 PI Komoriya A, Packard BS;
 XX
 XX WPI; 2001-389573/41.
 XX
 XX New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.

XX PS Claim 4; Page 71; 86pp; English.

XX CC The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention

XX SQ Sequence 18 AA;

Query Match 76.9%; Score 30; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDGIN 7
Db 8 HDGIN 12
|||||

RESULT 17

AAG73234

ID AAG73234 standard; peptide; 18 AA.

XX AC AAG73234;

XX DT 14-AUG-2001 (first entry)

XX DE Protease binding site #168.

XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; haemophilia.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT FT /note= "modified by fluorophore"

XX WO200118238-A1.

XX PD 15-MAR-2001.

XX PF 11-SEP-2000; 2000WO-US024882.

XX PR 10-SEP-1999; 99US-00394019.

XX PA (ONCO-) ONCOMUNIN INC.

XX PI Komoriya A, Packard BS;

XX DR WPI; 2001-389573/41.

XX CC New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samples.

XX PS Disclosure; Page 29; 86pp; English.

XX CC The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention

XX SQ Sequence 18 AA;

Query Match 76.9%; Score 30; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDGIN 7
Db 8 HDGIN 12
|||||

RESULT 18

AAY15690

ID AAY15690 standard; peptide; 5 AA.

XX AC AAY15690;

XX DT 27-JUL-1999 (first entry)

XX DE Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis; protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent; cell death; viral protease activity.

XX OS Synthetic.

XX PN WO9918856-A1.

XX PD 22-APR-1999.

XX PF 09-OCT-1998; 98WO-US021231.

XX PR 10-OCT-1997; 97US-0061582P.

XX PR 03-MAR-1998; 98US-00033661.

XX PA (CYTO-) CYTOVIA INC.

XX PI Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;

XX DR WPI; 1999-312448/26.

XX PT New fluorogenic or fluorescent reporter molecules.

XX PS Disclosure; Page 179; 202pp; English.

XX CC AAY15618-Y15759 represent peptides used to make the fluorogenic or fluorescent reporter molecules of the invention. These molecules contain a peptide moiety (e.g. present sequence) which acts as a substrate for enzymes involved in apoptosis or protease or peptidase enzymes. The compounds can be used as fluorogenic or fluorescent substrates for enzymes. Depending on the peptide moiety used, the fluorescent molecules can be used for detecting or measuring the activity of an enzyme involved in the apoptosis cascade in cells, to determine whether a test compound has an effect on an enzyme involved in the apoptosis cascade in cells; for determining the sensitivity of an animal with cancer to treatment with chemotherapeutic agents or determining whether a test substance inhibits, prevents, causes or enhances cell death of test cells; for detecting or measuring the activity of a viral protease in cells; for determining whether a test compound has an effect on the activity of a viral protease in cells; and for measuring the activity or determining whether a test substance has an effect on the activity of a protease or peptidase in cells

XX SQ Sequence 5 AA;

Query Match 74.4%; Score 29; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDG 5
|||||

Db 1 LEHDG 5

RESULT 19

AAG73287

ID AAG73287 standard; peptide; 7 AA.

AC AAG73287;

DT 14-AUG-2001 (first entry)

DE Protease indicator compound peptide #16.

XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;

KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;

KW haemophilia.

OS Synthetic.

XX WO200118238-A1.

PN 15-MAR-2001.

PD 11-SEP-2000; 2000WO-US024882.

PF 10-SEP-1999; 99US-00394019.

PR (ONCO-) ONCOIMMUNIN INC.

PA Komoriya A, Packard BS;

PI WPI; 2001-389573/41.

DR New fluorogenic compositions whose fluorescence level increases in the

XX presence of active proteases, useful for detecting and localizing

PT protease activity in biological samples, particularly in frozen tissue

PT samples.

XX Claim 1; Page 70; 86pp; English.

PS The present invention describes fluorogenic compositions which can be

CC used for the detection of protease activity. This can be useful as an

CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,

CC thrombosis and arthritis. The fluorogenic compositions comprise a

CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The

CC peptide is cleaved by a protease and the fluorophores can then be

CC detected. The present sequence is one of the peptides described in the

CC exemplification of the invention

XX Sequence 7 AA;

Query Match 74.4%; Score 29; DB 4; Length 7;

Best Local Similarity 85.7%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHDGIN 7

Db 1 LETDGIN 7

RESULT 20

ABU60443

ID ABU60443 standard; peptide; 7 AA.

XX ABU60443;

AC 29-APR-2003 (first entry)

DT Protease binding peptide motif SEQ ID 167.

XX Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;

KW nuclease; screening; fluorophore; substrate cleavage.

XX

OS Synthetic.

XX WO200261038-A2.

XX 08-AUG-2002.

PD 21-DEC-2001; 2001WO-US049781.

PF 22-DEC-2000; 2000US-00747287.

PR (ONCO-) ONCOIMMUNIN INC.

PA Packard BS, Komoriya A;

PI WPI; 2002-698548/75.

DR Indicator composition comprising polypeptide or nucleic acid backbone

XX joining two same chromophores resulting in quenching of fluorescence

PT of/change in absorbance of chromophores, useful for detecting protease

PT activity.

XX Disclosure; Page 35; 97pp; English.

PS This invention describes a novel indicator composition (referred as homo-

XX doubly labeled compositions) comprising a polypeptide backbone or a

CC nucleic acid backbone joining two chromophores of the same species

CC whereby the chromophores form an H-dimer resulting in quenching of the

CC fluorescence of or a change in the absorbance of the chromophore, a

CC decrease in fluorescence or a change in absorbance indicates that the

CC first molecule and the second molecule are interacting. The indicator is

CC useful for detecting the activity of a protease, where an increase in

CC fluorescence or a change in absorbance indicates that the protease

CC cleaves the polypeptide backbone. The indicator is attached to a solid

CC support inside a mammalian, yeast or insect cell. The composition bears a

CC hydrophobic group such as Fmoc, 9-fluorenylmethyl group, 1-fluorenone-1-

CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 4-fluorenone-1-

CC carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-

CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3,6-trimethyl-

CC benzene-sulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-

CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is

CC useful for detecting protease or nuclease activity (or the presence of

CC nucleic acid) in histological section, cells in culture, (e.g., seeded or

CC cultured adherent cells), a biological sample such as tissue, biopsy,

CC lymph, embryo, or whole animal, or cell suspension derived from a

CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.

CC The indicator composition is also useful for screening a test agent for

CC the ability to modulate a protease (or a nuclease, lipase, etc.). The

CC indicator reagents allow rapid determination of protease activity in a

CC matter of minutes in a single-step procedure. The fluorescent indicators

CC both absorb and emit in the visible range (400-800 nm). These signals are

CC therefore not readily quenched by, nor is activation of the fluorophores,

CC that is, absorption of light, interfered with by background molecules;

CC therefore they are easily detected in biological samples. The fluorogenic

CC protease indicators utilise high efficiency fluorophores and are able to

CC achieve a high degree of quenching while providing a strong signal when

CC the quench is released by cleavage of the peptide substrate. The high

CC signal allows detection of very low levels of protease activity. Thus the

CC fluorogenic protease indicators are particularly well suited for in situ

CC detection of protease activity. ABU60357-ABU60477 represent peptides use

CC to illustrate the method described in the disclosure of the invention

XX Sequence 7 AA;

Query Match 74.4%; Score 29; DB 5; Length 7;

Best Local Similarity 85.7%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHDGIN 7

Db 1 LETDGIN 7

RESULT 21

AAG73231
ID AAG73231 standard; peptide; 18 AA.
AC AAG73231;
XX
XX 14-AUG-2001 (first entry)
XX
XX Protease binding site #165.
XX
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
XX Synthetic.
OS
OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= OTHER
FT /note= "modified by fluorophore"
FT
FN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-US024882.
XX
XX 10-SEP-1999; 99US-00394019.
XX (ONCO-) ONCOIMMUNIN INC.
PA
PI Komoriya A, Packard BS;
XX
XX WPI; 2001-389573/41.
DR
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
XX Disclosure; Page 29; 86pp; English.
PS
XX The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 18 AA;

Query Match 74.4%; Score 29; DB 4; Length 18;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|||
DB 6 LETDGIN 12

RESULT 22
AAG73325
ID AAG73325 standard; peptide; 18 AA.
XX
XX AAG73325;
AC
XX

DT 14-AUG-2001 (first entry)
XX

DE Protease indicator compound peptide #54.
XX

KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;

KW haemophilia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT /label= OTHER
FT /note= "designated J in the specification"
FT
FT Modified-site 14
FT /label= OTHER
FT /note= "designated J in the specification"
XX
FN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-US024882.
XX
XX 10-SEP-1999; 99US-00394019.
XX (ONCO-) ONCOIMMUNIN INC.
PA
PI Komoriya A, Packard BS;
XX
XX WPI; 2001-389573/41.
DR
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
XX Claim 4; Page 71; 86pp; English.
PS
XX The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 18 AA;

Query Match 74.4%; Score 29; DB 4; Length 18;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|||
DB 6 LETDGIN 12

RESULT 23
ABB89029
ID ABB89029 standard; peptide; 20 AA.
XX
XX ABB89029;
AC
XX

DT 20-JUN-2002 (first entry)
XX

DE Babesia microti antigenic epitope fusion protein peptide BMN N term 4.
XX
XX Protozoacide; vaccine; antigen; antigenic epitope; infection.
KW
XX Babesia microti.
OS
XX WO200185947-A2.
PN
XX 15-NOV-2001.
PD
XX 09-MAY-2001; 2001WO-US015192.
PF
XX

PR 10-MAY-2000; 2000US-00569098.
PR 27-JUN-2000; 2000US-00605924.
PR 07-SEP-2000; 2000US-00656688.
PR 10-OCT-2000; 2000US-00685436.
PR 13-DEC-2000; 2000US-00737178.
PR 26-FEB-2001; 2001US-00794764.
XX (CORI-) CORIXA CORP.
PA
XX
XX
FI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer MJ;
PI Secrist H;
XX
XX WPI; 2002-216691/27.
DR
XX
XX
XX
XX
PT New Babesia microti antigens, useful for diagnosing and treating B.
PT microti infection, and as component of a composition for enhancing immune
PT response against B. microti infections.
XX
XX
XX Claim 2; Page 193; 195pp; English.
XX
XX The present invention relates to novel Babesia microti antigens and their
CC coding sequences. The B. microti antigens, antigenic epitopes of such
CC antigens, and compositions comprising such antigens are useful for
CC diagnosing and treating B. microti infection. The compositions are
CC especially useful for enhancing immune response against B. microti
CC infection. The present sequence was used to illustrate the invention
XX
XX
SQ Sequence 20 AA;
Query Match 74.4%; Score 29; DB 5; Length 20;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
QY 2 EHDGIN 7
Db |||||
6 EHDNIN 11
RESULT 24
ADE06161
ID ADE06161 standard; peptide; 20 AA.
XX
XX AC ADE06161;
XX
DT 29-JAN-2004 (first entry)
XX
XX
XX BMNI-related peptide #31.
XX
XX BMNI: immune response; Babesia microti infection; immunostimulant;
XX antiparasitic; Babesia microti antigen.
XX Babesia microti.
XX
XX US2003109689-A1.
XX
XX
XX 12-JUN-2003.
XX
XX 09-MAY-2001; 2001US-00853079.
XX
XX 01-OCT-1996; 96US-00723142.
PR 24-APR-1997; 97US-00845258.
PR 11-DEC-1997; 97US-00990571.
PR 05-APR-1999; 99US-00286488.
PR 17-MAR-2000; 2000US-00528784.
PR 10-MAY-2000; 2000US-00569098.
PR 27-JUN-2000; 2000US-00605724.
PR 07-SEP-2000; 2000US-00656688.
PR 10-OCT-2000; 2000US-00685436.
PR 13-DEC-2000; 2000US-00737178.
PR 26-FEB-2001; 2001US-00794764.
XX
XX (REED/) REED S G.
PA (LODE/) LODES M J.

PA (HOUG/) HOUGHTON R L.
PA (SLEA/) SLEATH P R.
PA (MCNE/) MCNEILL P D.
PA (HOME/) HOMER M J.
PA (SECR/) SECRIST H.
XX
XX Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer MJ;
PI Secrist H;
XX
XX WPI; 2003-801279/75.
DR
XX
XX
XX
XX
XX New isolated polynucleotide for stimulating an immune response in a
XX patient and/or for treating or detecting a Babesia microti infection.
XX
XX Claim 10; SEQ ID NO 215; 167pp; English.
XX
XX The invention relates to Babesia microti polynucleotides and the
CC polypeptides they encode. The polypeptides, antibodies specific for the
CC polypeptides and fusion proteins comprising the polypeptides are used
CC with immunostimulants for stimulating an immune response in a patient and
CC for treating a Babesia microti infection in a patient. Oligonucleotides
CC are used to diagnose B. microti infection in a patient by contacting a
CC biological sample from the patient with the oligonucleotide, detecting an
CC amount of binding of a polynucleotide that hybridises to the
CC oligonucleotide and comparing the amount of the polynucleotide that
CC hybridises to the oligonucleotide to a cut-off value. This sequence
CC represents a Babesia microti antigen (BMNI)-related peptide of the
CC invention.
XX
XX
SQ Sequence 20 AA;
Query Match 74.4%; Score 29; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 EHDGIN 7
Db |||||
6 EHDNIN 11
RESULT 25
AAG07964
ID AAG07964 standard; protein; 38 AA.
XX
XX AC AAG07964;
XX
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 5316.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 74.4%; Score 29; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDEI 6
Db 9 LEHDEI 14

RESULT 26
ID AAY55707 standard; protein; 39 AA.
AC AAY55707;
XX
XX
DT 07-FEB-2000 (first entry)
DE M. leprae ycfB peptide motif 4.
KW ycfB polypeptide; gram negative bacteria; gram positive bacteria;
KW antibacterial; bacterial infection; bacterial viability; antibiotic.
XX
XX Mycobacterium leprae.
XX
XX WO9954462-A2.
XX
XX 28-OCT-1999.
XX
XX 20-APR-1999; 99WO-EP002638.
XX
XX 22-APR-1998; 98GB-00008350.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Arigoni F, Edgerton MD, Loferer H, Peitsch MC;
XX
XX WPI; 2000-013249/01.
XX
XX Novel bacterial polypeptides used to identify broad spectrum antibiotics.
XX
XX Claim 3; Fig 2D; 56pp; English.
XX
XX The invention discloses a novel family of polypeptides, designated the
XX ycfB family, required for the growth of both gram negative and gram
XX positive bacteria. The novel polypeptide of ycfB family is defined by:
XX (a) a HSP score of greater than or equal to 100 when compared with one of
XX the amino acid sequences of the ycfB family members given in the
XX specification, when the BLAST algorithm is used with a BLOSUM62 scoring
XX matrix; (b) containing a set of amino acid sequences which are positively
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CC identified when position dependent scoring matrices according to tables 1
CC -4 (given in the specification) are used to yield a p-value of less than
CC 110-60; or (c) comprising any one of the sequences shown in AAY55710.
CC 711. The ycfB polypeptides and polynucleotides can be used in method to
CC identify antagonists and antibacterial compounds. These antagonists and
CC compounds can be used to treat bacterial infections. The polypeptides of
CC the invention are essential proteins for bacterial viability, and
CC represent new targets for antibiotics. Sequences AAY55647-709 represent
CC different motifs of the ycfB family polypeptides of various bacterial
CC species
XX
XX Sequence 39 AA;
SQ
Query Match 74.4%; Score 29; DB 3; Length 39;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
Db 13 EHDGVH 18

RESULT 27
AAW60953
ID AAW60953 standard; protein; 40 AA.
XX
XX AC AAW60953;
XX
XX DT 13-OCT-1998 (first entry)
XX
XX DE Streptococcus pneumoniae encoded polypeptide.
XX
XX coding region; ORF; open reading frame; antibacterial; infection;
XX prevention; meningitis.
XX
XX Streptococcus pneumoniae.
XX
XX WO9819689-A1.
XX
XX PD 14-MAY-1998.
XX
XX 27-OCT-1997; 97WO-US019226.
XX
XX 01-NOV-1996; 96US-0029930P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
XX Reid RH, Zarfos PN;
XX
XX WPI: 1998-286586/25.
XX
XX N-PSDB; AAV37353.
XX
XX New isolated nucleic acids from Streptococcus pneumoniae - useful, e.g.
XX for identifying anti-bacterial(s) for treatment and prevention of
XX meningitis.
XX
XX Claim 11; Page 54; 130pp; English.
XX
XX The sequence is that of the polypeptide encoded by a region isolated from
XX S. pneumoniae which shows homology to glutamate racemase. The protein, or
XX agonists of it, may be useful as an antibacterial for treatment or
XX prevention of infection, specifically caused by S. pneumoniae
XX (particularly meningitis) but possibly also Helicobacter pylori (ulcers
XX and gastric cancer). It may be of particular use before insertion of an
XX in-dwelling device or any other invasive procedure. The protein, or
XX nucleic acid encoding it, can also be used in vaccines to induce a
XX cellular and/or humoral immune response, or to screen for other
XX antibacterials. The DNA may also contain flanking sequences that are
XX potential sources of control elements for bacterial gene expression.
XX Detecting a sequence encoding the protein can be used diagnostically,
XX e.g. to detect a mutation for serotyping or classifying infectious agents
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XX      Sequence 40 AA;
SQ
  Query Match          74.4%; Score 29; DB 2; Length 40;
  Best Local Similarity 57.1%; Pred. NO. 1.2e+02;
  Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEHDGIN 7
DB      |||::|:
      22 LEHGVGD 28

RESULT 28
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ID      AAG07962 standard; protein; 52 AA.
XX
AC      AAG07962;
XX
DT      17-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana protein fragment SEQ ID NO: 5314.
XX
KW      Protein identification; signal transduction pathway; metabolic pathway;
KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
XX
OS      Arabidopsis thaliana.
XX
FN      EP1033405-A2.
XX
PD      06-SEP-2000.
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PF      25-FEB-2000; 2000EP-00301439.
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Query Match 74.4%; Score 29; DB 3; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 9 LEHEGI 14

RESULT 30
AAR37963

ID XX AAR37963 standard; protein; 64 AA.
 AC AAR37963;
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1993 (first entry)
 DE KGFR Ig-like domain 3 V-region inserted into FGFR2 framework.
 KW Polymerase chain reaction; immunoglobulin-like domain; tumour;
 KW ligand specificity region; LSK; fibroblast growth factor receptor;
 KW variable region; keratinocyte growth factor receptor; chimera.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Region 1..52
 FT Region /note= "mouse KGFR Ig-like domain 3 V-region"
 FT Region 53..64
 FT Region /note= "FGFR2 framework"
 FN EP545343-A1.
 PD 09-JUN-1993.
 PF 30-NOV-1992; 92EP-00120425.
 PF 02-DEC-1991; 91IL-00100219.
 PR (YEDA) YEDA RES & DEV CO LTD.
 PR Yayon A, Givol D;
 PR WPI; 1993-184106/23.
 DR N-PSDB; AAR37963.
 XX
 PT Ligand-binding domains of fibroblast growth factor receptor - used in
 PT chimeric proteins, inhibit proliferation of tumour cells.
 XX Example 1; Fig 3; 20pp; English.
 XX
 CC To prepare chimeric KGFR/FGFR2, a cDNA corresponding to the KGFR-v region
 CC of Ig-like domain D3 was cloned from mouse skin RNA using the PCR primer
 CC AAQ43158. This primer overlaps the constant region and the KGFR variable
 CC region of D3. Sequence analysis of the PCR product and the chimeric
 CC construct confirmed their identity to the KGFR sequence in that region
 CC and the in-frame insertion of the variable segment (see AAQ43153 and
 CC AAR37963). (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 64 AA;
 Query Match 74.4%; Score 29; DB 2; Length 64;
 Best Local Similarity 71.4%; Pred.No.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEHDSIN 7
 Db 1 LKHSGIN 7
 RESULT 31
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 ID AAM84389 standard; protein; 66 AA.
 AC AAM84389;
 XX
 XX
 DT 07-NOV-2001 (first entry)
 DE Human immune/haematopoietic antigen SEQ ID NO:11982.
 DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX

OS Homo sapiens.
 XX WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001354.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
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PR 05-JAN-2001; 2001US-0255967P.
PR (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-483426/52.
DR N-FSDB; AAK57170.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 11982; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX Sequence 66 AA;
SQ
Query Match 74.4%; Score 29; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 0; Indels 0;
QY 1 LEHDG 5
Db |||||
56 LEHDG 60
RESULT 32
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XX AAG49407;
AC
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 62502.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62502.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
PN 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
PF
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Query Match 74.4%; Score 29; DB 3; Length 67;
Best Local Similarity 83.3%; Pred. No. 2,1e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCI 6
Db 23 LEHEGI 28

RESULT 33
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XX
AC AAG34647;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42192.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145152P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 26-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149727P.
PR 23-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 25-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150586P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156456P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.

PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 74.4%; Score 29; DB 3; Length 74;
Best Local Similarity 83.3%; Pred. NO. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDTG 6
DB 3 LEHDTG 8

RESULT 34
ABP80959
ID ABP80959 standard; protein; 82 AA.
XX
AC ABP80959;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 8448.
XX
KW Antibacterial; infection; vaccine; gene therapy.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200279243-A2.
XX
PD 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana MR, Pizza M, Masignani V, Monaci E;
XX
WPI: 2003-058415/05.
XX
N-PSDB; AB241929.

New protein from Neisseria gonorrhoeae, useful for the manufacture of a
medicament for treating or preventing N. gonorrhoeae infection.
Disclosure; Page 803; 815pp; English.

The present invention relates to proteins from Neisseria gonorrhoeae.
Also disclosed are the nucleic acid molecules encoding the proteins and
antibodies that specifically bind to the proteins. The composition
comprising the protein, nucleic acid or antibody is useful for the
manufacture of a medicament for treating or preventing N. gonorrhoeae
infection, this may be in the form of a vaccine or gene therapy.
Sequences given in records ABP76736-ABP81046 represent nucleic acid
molecules of the invention

XX Sequence 82 AA;
Query Match 74.4%; Score 29; DB 6; Length 82;
Best Local Similarity 66.7%; Pred. NO. 2.6e+02;
```

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 BHDGIN 7
|:|:|
DB 64 BHGVN 69

RESULT 35
ADC95330
ID ADC95330 standard; protein; 83 AA.

XX AC ADC95330;
XX 01-JAN-2004 (first entry)
XX E. faecium protein sequence SEQ ID 4957.
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX Enterococcus faecium.
OS US6583275-B1.
PN 24-JUN-2003.
XX 30-JUN-1998; 98US-00107532.
XX 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Doucette-Stamm LA, Bush D;
PI WPI: 2003-799836/75.
DR N-PSDB; ADC91676.
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX Example 1; SEQ ID NO 4957; 243pp; English.

XX The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridizing to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX Sequence 83 AA;

Query Match 74.4%; Score 29; DB 7; Length 83;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGI 6
|:|:|
DB 57 LKHDGI 52

RESULT 36
ABP64017
ID ABP64017 standard; protein; 84 AA.

XX AC ABP64017;
XX 04-NOV-2002 (first entry)
XX Human ORF387.
XX Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulneryary;
KW Antinflammatory; gene therapy; human; ORFX; atherogenic; platelet;
KW human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
KW cancer; cardiovascular disease; allergy; autoimmune disease;
KW wound healing; blood coagulation disorder; inflammatory disorder.

XX Homo sapiens.
OS US2002082206-A1.
PN 27-JUN-2002.
XX 30-MAY-2001; 2001US-00867550.
XX 30-MAY-2000; 2000US-0208427P.
XX (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.

XX Leach MD, Mehraban F, Conley PB, Topper JN, Law D;
PI WPI: 2002-626554/67.
DR N-PSDB; ABQ98580.
XX New polypeptide designated ORFX are present in human atherogenic cells
PT and are useful to prevent and treat ORFX-associated disorders including
PT cancer, allergy, wound healing or autoimmune, cardiovascular or
PT inflammatory disease.
XX Claim 10; SEQ ID NO 774; 78pp; English.

XX The present invention relates to novel human ORFX polypeptides and their
CC coding sequences (ABP63631-ABP64631 and ABQ98194-ABQ99267). The sequences
CC were discovered in human atherogenic cells, in particular in platelets
CC and human umbilical vein endothelial cells (HUVEC) and are expressed in
CC many other tissues as well. Atherogenic cells are cells which have the
CC potential to develop atherosclerotic plaques. The ORFX polypeptides and
CC nucleic acids are useful for treating or preventing a pathological
CC condition associated with an ORFX-associated disorder, e.g. cancer, blood
CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood
CC coagulation disorders or inflammatory disorders. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/sequence.html?DocID=2002082206

XX Sequence 84 AA;
Query Match 74.4%; Score 29; DB 5; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|:|
DB 29 LEHDG 33

RESULT 37
AAG34646

ID	AAG34646	standard; protein; 87 AA.
XX	XX	
AC	AAG34646;	
XX	XX	
DT	18-OCT-2000	(first entry)
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 42191.
XX	XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	XX	
OS	Arabidopsis thaliana.	
XX	XX	
PN	EP1033405-A2.	
XX	XX	
PD	06-SEP-2000.	
XX	XX	
PF	25-FEB-2000;	2000EP-00301439.
XX	XX	
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127452P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130891P.
PR	28-APR-1999;	99US-0131449P.
PR	30-APR-1999;	99US-0132048P.
PR	30-APR-1999;	99US-0132407P.
PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	06-MAY-1999;	99US-0132487P.
PR	07-MAY-1999;	99US-0132863P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135154P.
PR	21-MAY-1999;	99US-0135633P.
PR	24-MAY-1999;	99US-0135639P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138847P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139492P.
PR	18-JUN-1999;	99US-0139454P.
PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139458P.
PR	18-JUN-1999;	99US-0139459P.
PR	18-JUN-1999;	99US-0139460P.

PR 23-AUG-1999; 99US-0149910P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159323P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160982P.
 PR 22-OCT-1999; 99US-0160983P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

 Query Match 74.4%; Score 29; DB 3; Length 87;
 Best Local Similarity 83.3%; Pred. No. 2, 8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 LEHDSGI 6
 Db 16 LEHEGI 21

 RESULT 38
 AAE32812
 ID AAE32812 standard; peptide; 92 AA.
 AC AAE32812;
 XX
 XX 24-MAR-2003 (first entry)
 DT
 XX Human CEA exon #15 encoded peptide.

XX Human; carcinoembryonic antigen; CEA; cell adhesion-mediated disease;
 KW prognosis; cancer; tumour; gene therapy; exon.
 XX Homo sapiens.
 XX WO20020508-A2.
 XX 14-NOV-2002.
 XX 07-MAY-2002; 2002WO-US014457.
 XX 07-MAY-2001; 2001US-0289179P.
 XX 29-AUG-2001; 2001US-0315736P.
 XX (ALPH-) ALPHAGENE INC.
 XX Stark KA, Weaver A, Hoffmann HM, Krauss R, Valenzuela DB;
 PI Saini KS;
 XX WPI; 2003-111965/10.
 DR N-PSDB; AAD50563.
 XX
 PT New carcinoembryonic antigen and polynucleotides encoding them, useful
 PT for treating and/or preventing cell adhesion-mediated disease (e.g.
 PT cancers, solid tumors, tumor metastasis or benign tumors) symptoms.
 XX Claim 17; Page 127; 143pp; English.
 XX The invention relates to novel human carcinoembryonic antigen (CEA)
 CC polypeptides and polynucleotides encoding such polypeptides. CEA genes
 CC are useful as diagnostic and prognostic markers of colon, stomach and
 CC breast cancers. Polypeptides of the invention can be used to diagnose,
 CC treat and/or prevent cell adhesion-mediated disease (e.g. cancers, solid
 CC tumours, tumour metastasis or benign tumours) and to modulate cell-cell
 CC or cell-matrix adhesion in mammalian tissues. The invention is useful in
 CC gene therapy. The present sequence is human CEA exon encoded peptide
 XX Sequence 92 AA;
 SQ

 Query Match 74.4%; Score 29; DB 6; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 EHDGI 6
 Db 65 EHDGI 69

 RESULT 39
 AAU52002
 ID AAU52002 standard; protein; 103 AA.
 XX
 AC AAU52002;
 XX
 XX 27-FEB-2002 (first entry)
 DT
 XX Propionibacterium acnes immunogenic protein #12898.
 DE
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 XX WO200181581-A2.
 XX
 XX 01-NOV-2001.
 XX
 XX 20-APR-2001; 2001WO-US012865.
 XX
 XX 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
DA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI: 2001-616774/71.
DR N-PSDB; AAS59553.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
PS Example 1; SEQ ID NO 13197; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 103 AA;
Query Match 74.4%; Score 29; DB 4; Length 103;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HDGIN 7
Db 2 HDGVN 6
RESULT 40
ID AEM48521
XX AEM48521 standard; protein; 103 AA.
XX
AC AEM48521;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #13197.
XX
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.

XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Valiieve-Douglas J;
XX
XX WPI: 2003-381789/36.
DR N-PSDB; ACF64482.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 13197; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 103 AA;
Query Match 74.4%; Score 29; DB 6; Length 103;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HDGIN 7
Db 2 HDGVN 6
RESULT 41
ID AAU57868
XX AAU57868 standard; protein; 106 AA.
XX
AC AAU57868;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #18764.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
XX 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.
XX PR
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
XX PR (CORI-) CORIXA CORP.
XX PA
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX PR
XX PR WPI; 2001-616774/71.
XX PR N-PSDB; AAS95587.
XX PR
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX PR
XX PR Example 1; SEQ ID NO 19063; 1069pp; English.
XX PS
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 106 AA;
Query Match 74.4%; Score 29; DB 4; Length 106;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HDGIN 7
Db 6 HDGVN 10
|||
|||
RESULT 42
ABG15770
ID ABG15770 standard; protein; 106 AA.
XX AC
XX AC ABG15770;
XX DT
XX DT 18-FEB-2002 (first entry)
XX DE
XX DE Novel human diagnostic protein #15761.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS
XX OS Homo sapiens.
XX XX
XX PN WO200175067-A2.
XX PD
XX PD 11-OCT-2001.
XX PF
XX PF 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PR
XX PA (HYSE-) HYSEQ INC.
XX XX
XX PI Drmanac RT, Liu C, Tang YT;
XX XX
XX XX WPI; 2001-639362/73.
XX DR N-PSDB; AAS79957.
XX DR
XX PR New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PR
XX PS Claim 20; SEQ ID NO 46129; 103pp; English.
XX CC
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 106 AA;
Query Match 74.4%; Score 29; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGI 6
Db 55 EHDGI 59
RESULT 43
ABM54387
ID ABM54387 standard; protein; 106 AA.
XX AC
XX AC ABM54387;
XX DT
XX DT 20-OCT-2003 (first entry)
XX XX
XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #19063.
XX KW
XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunostimulant; immune response; vaccine.
XX XX
XX OS Propionibacterium acnes.
XX XX
XX PN WO2003033515-A1.
XX XX
XX PD 24-APR-2003.
XX XX
XX PF 11-OCT-2002; 2002WO-US032727.
XX XX
XX PF 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliave-Douglas J;
 XX DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64516.
 XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 19063; 1481pp; English.
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 106 AA;
 Query Match 74.4%; Score 29; DB 6; Length 106;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDGIN 7
 DB 6 HDGVN 10
 |||||
 RESULT 44
 ABG27666
 ID ABG27666 standard; protein; 107 AA.
 XX AC ABG27666;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #27657.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 PD

XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS91853.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 58025; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 107 AA;
 Query Match 74.4%; Score 29; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEHDG 5
 DB 31 LEHDG 35
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 RESULT 45
 ABG93329
 ID ABG93329 standard; protein; 113 AA.
 XX AC ABG93329;
 XX DT 21-NOV-2002 (first entry)
 XX DE C. albicans BAX-associated protein fragment SEQ ID 616.
 XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
 KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
 KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
 KW neurodegeneration; cell death.
 XX OS Candida albicans.
 XX WO200264766-A2.
 XX 22-AUG-2002.
 PD

XX 21-DEC-2001; 2001WO-EP015398.
 PF XX
 XX 22-DEC-2000; 2000EP-00870318.
 PR 04-JAN-2001; 2001EP-00870002.
 PR 09-JAN-2001; 2001EP-00870003.
 XX (JANC) JANSSEN PHARM NV.
 PA Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
 XX
 PI WPI; 2002-667002/71.
 XX N-PSDB; ABQ76595.
 DR
 DR
 XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
 PT medicament for treating, preventing and/or alleviating yeast or fungal
 PT infections or proliferative disorders, or for preventing apoptosis in
 PT certain diseases.
 XX
 XX Claim 36; Fig 2; 344pp; English.
 PS
 XX This invention describes a novel nucleic acid representing a synthetic
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
 CC resistant yeast or fungi, identifying, or obtaining and identifying
 CC Candida spp. sequences that are differentially expressed in a pathway
 CC eventually leading to programmed cell death or identifying inhibitors or
 CC inhibitor sequences of Bax-induced cell death. The products of the
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and
 CC vasotropic activity and can be used in vaccines or for gene therapy. The
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
 CC antisense molecules and antibodies are useful as medicaments or in
 CC preparing a medicament for treating, preventing and/or alleviating
 CC diseases associated with yeast or fungi or proliferative disorders, such
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds
 CC or polypeptides, or the genetically modified organism are useful for
 CC preparing a medicament for modifying the endogenic flora of humans and
 CC other mammals. The vaccine is useful for immunising against yeast or
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,
 CC ischaemia, diseases related with viral infections or neurodegenerations.
 CC This sequence represents a polypeptide associated with the Bax gene
 CC described in the disclosure of the invention
 XX
 SQ Sequence 113 AA;
 Query Match 74.4%; Score 29; DB 5; Length 113;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGIN 7
 Db ||:|:
 58 EHEGLN 63
 Search completed: June 15, 2004, 12:25:20
 Job time : 56 secs

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OM protein - protein search, using sw model

Run on: June 15, 2004, 12:22:52 ; Search time 23 Seconds
(without alignments)
15,712 Million cell updates/sec

Title: US-09-394-019C-212

Perfect score: 39

Sequence: 1 LEHGDIN 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 290705

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.psp.*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.psp.*
- 3: /cgn2_6/ptodata/2/iaa/6A-COMB.psp.*
- 4: /cgn2_6/ptodata/2/iaa/6B-COMB.psp.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.psp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	76.9	109	2	US-08-470-670A-11
2	30	76.9	109	4	US-08-461-511A-11
3	29	74.4	5	4	US-09-521-650-73
4	29	74.4	5	4	US-09-168-888-73
5	29	74.4	83	4	US-09-107-532A-4957
6	29	74.4	86	4	US-09-134-000C-6650
7	29	74.4	142	4	US-09-543-681A-7907
8	28	71.8	116	1	US-08-497-035-4
9	27	69.2	15	3	US-08-836-561-37
10	27	69.2	15	4	US-09-434-122-37
11	27	69.2	33	4	US-09-331-930A-16
12	27	69.2	33	4	US-09-331-930A-18
13	27	69.2	62	4	US-09-107-532A-6499
14	27	69.2	65	4	US-09-543-681A-6247
15	27	69.2	73	4	US-09-331-930A-2
16	27	69.2	73	4	US-09-331-930A-19
17	27	69.2	73	4	US-09-331-930A-20
18	27	69.2	73	4	US-09-331-930A-21
19	27	69.2	125	4	US-09-543-681A-8087
20	27	69.2	131	3	US-08-836-561-25
21	27	69.2	131	4	US-09-434-122-25
22	26	66.7	40	4	US-09-106-568E-131
23	26	66.7	67	4	US-08-938-165A-289
24	26	66.7	68	4	US-09-540-236-2048
25	26	66.7	70	4	US-09-621-976-4677
26	26	66.7	88	4	US-09-621-976-6918
27	26	66.7	109	4	US-09-325-932A-144

Sequence 4815, Ap
Sequence 5829, Ap
Sequence 2, Appl
Sequence 1, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 25109, A
Sequence 10461, A
Sequence 11391, A
Sequence 71, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 42, Appl

Query Match 76.9%; Score 30; DB 2; Length 109;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHGDIN 7

ALIGNMENTS

RESULT 1
US-08-470-670A-11
; Sequence 11, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-470-670A-11

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Db      | |||:|
        45 LFHDGVN 51

RESULT 2
US-08-461-511A-11
; Sequence 11, Application US/08461511A
; Patent No. 6303331
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.B.
;           Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
;           AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,511A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD.179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-461-511A-11

Query Match      76.9%; Score 30; DB 4; Length 109;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LEHDGIN 7
Db      45 LFHDGVN 51

RESULT 3
US-09-521-650-73
; Sequence 73, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888

; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-73

Query Match      74.4%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEHDG 5
Db      1 LEHDG 5

RESULT 4
US-09-168-888-73
; Sequence 73, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-73

Query Match      74.4%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEHDG 5
Db      1 LEHDG 5

RESULT 5
US-09-107-532A-4957
; Sequence 4957, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
```

```
;
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 4957:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...83
; SEQUENCE DESCRIPTION: SEQ ID NO: 4957:
US-09-107-532A-4957

Query Match 74.4%; Score 29; DB 4; Length 83;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDCI 6
Db 57 LKHDGI 62

RESULT 6
US-09-134-000C-6650
; Sequence 6650, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6650
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6650
```

```
Query Match 74.4%; Score 29; DB 4; Length 86;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 28 EHSGIN 33

RESULT 7
US-09-543-681A-7907
; Sequence 7907, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7907
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7907

Query Match 74.4%; Score 29; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGI 6
Db 31 EHDGI 35

RESULT 8
US-08-497-025-4
; Sequence 4, Application US/08497025
; Patent No. 5646251
; GENERAL INFORMATION:
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Rivas, Alberto
; APPLICANT: Laus, Reiner
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: ALLOREACTION-ASSOCIATED ANTIGEN (ARAg):
; TITLE OF INVENTION: A NOVEL MEMBER OF THE IMMUNOGLOBULIN GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,025
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/149,212
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
```



```

; REFERENCE/DOCKET NUMBER: 5490A-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..116
; OTHER INFORMATION: /note= "A variable-type
; OTHER INFORMATION: immunoglobulin-type domain of ARag-h-1."
US-08-497-025-4

Query Match 71.8%; Score 28; DB 1; Length 116;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCG 6
DB 52 LQHDGL 57

RESULT 9
US-08-836-561-37
; Sequence 37, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-434-122-37

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-561-37

Query Match 69.2%; Score 27; DB 3; Length 15;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCG 7
DB 6 VDHNGVN 12

RESULT 10
US-09-434-122-37
; Sequence 37, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6538111uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-NO. 6538111-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-434-122-37

Query Match 69.2%; Score 27; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCG 7
DB 6 VDHNGVN 12

```

Db 6 VDHNGVN 12

Sequence 6499, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Dereke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6499:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...62
SEQUENCE DESCRIPTION: SEQ ID NO: 6499:
US-09-107-532A-6499

Query Match 69.2%; Score 27; DB 4; Length 62;
Best Local Similarity 86.7%; Pred. No. 85;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 20 QHNGIN 25

RESULT 14
US-09-543-681A-6247
Sequence 6247, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6247

Db 6 VDHNGVN 12

Sequence 16, Application US/09331930A
Patent No. 6436670
GENERAL INFORMATION:
APPLICANT: ZIMMET, PAUL Z.
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT APPLICATION NUMBER: US/09/331,930A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: PCT/AU98/00902
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: AU PP0117/97
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: AU PP0323/97
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 33
TYPE: PRT
ORGANISM: Psammomys obesus
US-09-331-930A-16

Query Match 69.2%; Score 27; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDGIN 7
Db 23 HDGWN 27

RESULT 12
US-09-331-930A-18
Sequence 18, Application US/09331930A
Patent No. 6436670
GENERAL INFORMATION:
APPLICANT: ZIMMET, PAUL Z.
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT APPLICATION NUMBER: US/09/331,930A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: PCT/AU98/00902
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: AU PP0117/97
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: AU PP0323/97
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 33
TYPE: PRT
ORGANISM: Psammomys obesus
US-09-331-930A-18

Query Match 69.2%; Score 27; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDGIN 7
Db 23 HDGWN 27

RESULT 13
US-09-107-532A-6499

```
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6247

Query Match          69.2%; Score 27; DB 4; Length 65;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Gaps 0; Indels 2;
QY 1 LEHGIN 7
Db 25 LSHGVN 31

RESULT 15
US-09-331-930A-2
; Sequence 2, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-2

Query Match          69.2%; Score 27; DB 4; Length 73;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Gaps 0; Indels 0;
QY 3 HDGIN 7
Db 63 HDGMN 67

RESULT 16
US-09-331-930A-19
; Sequence 19, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-331-930A-21

Query Match          69.2%; Score 27; DB 4; Length 73;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Gaps 0; Indels 0;
QY 3 HDGIN 7
Db 63 HDGMN 67

RESULT 17
US-09-331-930A-20
; Sequence 20, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-331-930A-20

Query Match          69.2%; Score 27; DB 4; Length 73;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Gaps 0; Indels 0;
QY 3 HDGIN 7
Db 63 HDGMN 67

RESULT 18
US-09-331-930A-21
; Sequence 21, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-331-930A-21
```

Query Match 69.2%; Score 27; DB 4; Length 73;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
Db 63 HDGMN 67

US-09-543-681A-8087
Sequence 8087, Application US/09543681A
Patent No. 6505709
GENERAL INFORMATION:
APPLICANT: GARY BRTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8087
LENGTH: 125
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-8087

Query Match 69.2%; Score 27; DB 4; Length 125;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCI 6
Db 119 LEHGV 124

US-08-836-561-25
Sequence 25, Application US/08836561
Patent No. 6018032
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: IIDA, Akihiro
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995

Query Match 69.2%; Score 27; DB 3; Length 131;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCIN 7
Db 49 VDHGVN 55

US-08-836-561-25
Sequence 25, Application US/09434122
Patent No. 6538111
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: IIDA, Akihiro
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6538111uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,122
FILING DATE: 05-No. 6538111-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid

```
/
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-434-122-25

Query Match          69.2%; Score 27; DB 4; Length 131;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGGIN 7
Db 49 VDHNGVN 55

RESULT 22
US-09-106-568E-131 Application US/09106568E
; Sequence 131, Application US/09106568E
; Patent No. 6455248
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J.
; APPLICANT: Bhattacharjee, Kalavati
; APPLICANT: Bhattacharjee, Vasker
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/106,568E
; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 131
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of TYCA_BACR shown in Figure 4.
US-09-106-568E-131

Query Match          66.7%; Score 26; DB 4; Length 40;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGGI 6
Db 22 LEHGGI 27

RESULT 23
US-08-936-165A-289 Application US/08936165A
; Sequence 289, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
```

```
/
/ ZIP: 19406-0939
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/936,165A
/ FILING DATE: 24-SEP-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/027,032
/ FILING DATE: 24-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gimmil, Edward R
/ REGISTRATION NUMBER: 38,891
/ REFERENCE/DOCKET NUMBER: P50549
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-4478
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 289:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 67 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Protein
US-08-936-165A-289

Query Match          66.7%; Score 26; DB 4; Length 67;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGGI 6
Db 17 LEYDGV 22

RESULT 24
US-09-540-236-2048 Application US/09540236
; Sequence 2048, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRH
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2048
; LENGTH: 68
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2048

Query Match          66.7%; Score 26; DB 4; Length 68;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGGIN 7
Db 51 IKNDGIN 57

RESULT 25
US-09-621-976-4677 Application US/09621976
; Sequence 4677, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4677
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4677

Query Match 66.7%; Score 26; DB 4; Length 70;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDS 5
Db 48 LQHDG 52

RESULT 26
US-09-621-976-6918
; Sequence 6918, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6918
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6918

Query Match 66.7%; Score 26; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDS 6
Db 41 LEYDGV 46

RESULT 27
US-09-325-932A-144
; Sequence 144, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-144

Query Match 66.7%; Score 26; DB 4; Length 109;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 EHDGIN 7
Db 81 EHTGLN 86

RESULT 28
US-09-328-352-4815
; Sequence 4815, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 3252
; SEQ ID NO 4815
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4815

Query Match 66.7%; Score 26; DB 4; Length 113;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDS 6
Db 51 IKHDGV 56

RESULT 29
US-09-621-976-5829
; Sequence 5829, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5829
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -88..-1
US-09-621-976-5829

Query Match 66.7%; Score 26; DB 4; Length 113;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDS 7
Db 64 LEHDDVS 70

RESULT 30
US-08-047-033-2
; Sequence 2, Application US/08047033
; Patent No. 544157
; GENERAL INFORMATION:
; APPLICANT: FUJIO SUZUKI et al.
; TITLE OF INVENTION: CHONDROMODULIN-I PROTEIN

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,033
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,859
FILING DATE:
APPLICATION NUMBER: US/07/745,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: bovine
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: fetal cartilage
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 7
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Met or Val"
FEATURE:
NAME/KEY: modified site
LOCATION: 10
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Glu or Thr"
FEATURE:
NAME/KEY: modified site
LOCATION: 83
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Cys or Val"
PUBLICATION INFORMATION:

AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-2
Query Match 66.7%; Score 26; DB 1; Length 120;
Best Local Similarity 66.7%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;
QY 1 LEHDCI 6
Db 62 LDHEGI 67
RESULT 31
US-08-047-033-1
Sequence 1, Application US/08047033
Patent No. 5444157
GENERAL INFORMATION:
APPLICANT: Fujio SUZUKI et al.
TITLE OF INVENTION: CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,033
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,859
FILING DATE:
APPLICATION NUMBER: US/07/745,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: bovine
STRAIN:
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: fetal cartilage
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 7
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Met or Val"
FEATURE:
NAME/KEY: modified site
LOCATION: 10
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Glu or Thr"
FEATURE:
NAME/KEY: modified site
LOCATION: 84
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Xaa is Cys or Val"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-1

Query Match 66.7%; Score 26; DB 1; Length 121;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCI 6
|:|:|
Db 63 LDHEGI 68

RESULT 32
US-08-887-534A-76
; Sequence 76, Application US/08887534A
; Patent No. 6455323
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/887,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-527-431-76

Query Match 66.7%; Score 26; DB 4; Length 128;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-887-534A-76

Query Match 66.7%; Score 26; DB 4; Length 128;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|:|
Db 39 LQHDG 43

RESULT 33
US-09-527-431-76
; Sequence 76, Application US/09527431
; Patent No. 6485899
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/527,431
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/887,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-527-431-76

Query Match 66.7%; Score 26; DB 4; Length 128;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDG 5
Db 39 LQHDG 43

RESULT 34
US-08-392-828C-38
; Sequence 38 Application US/08392828C
; Patent No. 5795962
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAHI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO
; TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,828C
; FILING DATE: 28-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..137
; OTHER INFORMATION: /note= "XYN Z SEQUENCE (FIGURE 3)"
US-08-392-828C-38

Query Match 66.7%; Score 26; DB 1; Length 137;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 8 DYDGIN 13

RESULT 35
US-09-330-945-38
; Sequence 38 Application US/09330945
; Patent No. 6077946
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAHI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO

; TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
; TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT A
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/119,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: FUN-032DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..137
; OTHER INFORMATION: /note= "XYN Z SEQUENCE (FIGURE 3)"
US-09-330-945-38

Query Match 66.7%; Score 26; DB 3; Length 137;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 8 DYDGIN 13

RESULT 36
US-09-252-991A-25109
; Sequence 25109, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25109
; TYPE: PRT
; LENGTH: 139
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25109

Query Match	66.7%;	Score 26;	DB 4;	Length 139;
Best Local Similarity	83.3%;	Pred. No. 3.5e+02;		
Matches	5;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1 LEHDGI 6			
Db	82 LVHDGI 87			
RESULT 37				
US-09-489-039A-10461				
; Sequence 10461, Application US/09489039A				
; Patent No. 6610836				
; GENERAL INFORMATION:				
; APPLICANT: Gary Breton et. al				
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA				
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS				
; FILE REFERENCE: 2709.2004001				
; CURRENT APPLICATION NUMBER: US/09/489,039A				
; CURRENT FILING DATE: 2000-01-27				
; PRIOR APPLICATION NUMBER: US 60/117,747				
; PRIOR FILING DATE: 1999-01-29				
; NUMBER OF SEQ ID NOS: 14342				
; SEQ ID NO 10461				
; LENGTH: 142				
; TYPE: PRT				
; ORGANISM: Klebsiella pneumoniae				
US-09-489-039A-10461				
Query Match	66.7%;	Score 26;	DB 4;	Length 142;
Best Local Similarity	66.7%;	Pred. No. 3.6e+02;		
Matches	4;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;
QY	1 LEHDGI 6			
Db	15 IEHNGI 20			
RESULT 38				
US-09-489-039A-11391				
; Sequence 11391, Application US/09489039A				
; Patent No. 6610836				
; GENERAL INFORMATION:				
; APPLICANT: Gary Breton et. al				
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA				
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS				
; FILE REFERENCE: 2709.2004001				
; CURRENT APPLICATION NUMBER: US/09/489,039A				
; CURRENT FILING DATE: 2000-01-27				
; PRIOR APPLICATION NUMBER: US 60/117,747				
; PRIOR FILING DATE: 1999-01-29				
; NUMBER OF SEQ ID NOS: 14342				
; SEQ ID NO 11391				
; LENGTH: 147				
; TYPE: PRT				
; ORGANISM: Klebsiella pneumoniae				
US-09-489-039A-11391				
Query Match	66.7%;	Score 26;	DB 4;	Length 147;
Best Local Similarity	50.0%;	Pred. No. 3.7e+02;		
Matches	3;	Conservative	3;	Mismatches 0; Indels 0; Gaps 0;
QY	1 LEHDGI 6			
Db	46 IDHDGL 51			
RESULT 39				
US-09-521-650-71				
; Sequence 71, Application US/09521650				
; Patent No. 6335429				
; GENERAL INFORMATION:				

Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDG 5
Db 2 EHDG 5
RESULT 41
US-09-168-888-71
; Sequence 71, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-168-888-71
Query Match 64.1%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDG 5
Db 2 EHDG 5
RESULT 42
US-09-168-888-78
; Sequence 78, Application US/09168889
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78

LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-168-888-78
Query Match 64.1%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDG 5
Db 2 EHDG 5
RESULT 43
US-09-561-756-42
; Sequence 42, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease sensitive linker region between the small
; OTHER INFORMATION: and large subunits of a Rev-caspase
US-09-561-756-42
Query Match 64.1%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDG 5
Db 2 EHDG 5
RESULT 44
US-09-227-721-42
; Sequence 42, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease sensitive linker region between the small
; OTHER INFORMATION: and large subunits of a Rev-caspase
US-09-227-721-42
Query Match 64.1%; Score 25; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDG 5
|
|
|
|
Db 2 EHDG 5

RESULT 45

US-09-954-697-42
; Sequence 42, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease sensitive linker region between the small
; OTHER INFORMATION: and large subunits of a Rev-caspase
US-09-954-697-42

Query Match 64.1%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDG 5
|
|
|
|
Db 2 EHDG 5

Search completed: June 15, 2004, 12:26:30
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: June 15, 2004, 12:23:26 ; Search time 42 Seconds
(without alignments)
46.954 Million cell updates/sec

Title: US-09-394-019C-212

Perfect score: 39

Sequence: 1 LEHDGIN 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 581086

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	18	US-09-747-287-199	Sequence 199, App
2	39	100.0	18	US-09-874-350A-165	Sequence 165, App
3	39	100.0	18	US-09-874-350A-206	Sequence 206, App
4	35	89.7	18	US-09-747-287-201	Sequence 201, App
5	35	89.7	18	US-09-874-350A-167	Sequence 167, App
6	35	89.7	18	US-09-874-350A-207	Sequence 207, App
7	35	89.7	131	US-10-424-599-170453	Sequence 170453, App
8	33	84.6	76	US-10-424-599-284592	Sequence 284592, App
9	32	82.1	17	US-10-083-357-1105	Sequence 1105, App
10	31	79.5	30	US-09-270-983-4	Sequence 4, Appl
11	31	79.5	66	US-10-424-599-234026	Sequence 234026, App
12	30	76.9	18	US-09-747-287-203	Sequence 203, App
13	30	76.9	18	US-09-874-350A-169	Sequence 169, App
14	30	76.9	55	US-10-424-599-210542	Sequence 210542, App
15	30	76.9	70	US-10-424-599-160368	Sequence 160368, App

ALIGNMENTS

RESULT 1

US-09-747-287-199
Sequence 199, Application US/09747287
Publication No. US20030207264A1

GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES

FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287
CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 242
SOFTWARE: PatentIn version 3.2

SEQ ID NO 199
LENGTH: 18

TYPE: PRT
ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: Synthetic peptide.

NAME/KEY: misc feature
LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
NAME/KEY: misc feature
LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-199

Query Match 100.0%; Score 39; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;

Sequence 21259, A
Sequence 70959, A
Sequence 73, Appl
Sequence 200, App
Sequence 166, App
Sequence 215, App
Sequence 215, App
Sequence 774, App
Sequence 165583, A
Sequence 203990, A
Sequence 11679, A
Sequence 14258, A
Sequence 14594, A
Sequence 147562, A
Sequence 16, Appl
Sequence 29, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 89, Appl
Sequence 126, App
Sequence 130, App
Sequence 647, App
Sequence 647, App
Sequence 262285, A
Sequence 116, App
Sequence 208279, A
Sequence 222247, A
Sequence 215145, A
Sequence 216092, A

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEHGDGIN 7
Db 6 LEHGDGIN 12

RESULT 2

US-09-874-350A-165
; Sequence 165, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
US-09-874-350A-165

Query Match 100.0%; Score 39; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
Db 6 LEHGDGIN 12

RESULT 3

US-09-874-350A-206
; Sequence 206, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 206
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-206

Query Match 100.0%; Score 39; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
Db 6 LEHGDGIN 12

RESULT 4

US-09-747-287-201
; Sequence 201, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 201
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-201

Query Match 89.7%; Score 35; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
Db 7 EHDGIN 12

RESULT 5
US-09-874-350A-167
; Sequence 167, Application US/09874350A
; Publication No. US2004009626A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmun, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 167
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon aminocaproic acid
US-09-874-350A-167
Query Match 89.7%; Score 35; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDGIN 7
Db 7 EHDGIN 12
RESULT 6
US-09-874-350A-207
; Sequence 207, Application US/09874350A
; Publication No. US2004009626A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmun, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 167
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon aminocaproic acid
US-09-874-350A-167
Query Match 89.7%; Score 35; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDGIN 7
Db 7 EHDGIN 12
RESULT 7
US-10-424-599-170453
; Sequence 170453, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170453
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(131)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_124935C.1.pep
US-10-424-599-170453
Query Match 89.7%; Score 35; DB 12; Length 131;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EHDGIN 7
Db 106 EHDGIN 111
RESULT 8
US-10-424-599-284592
; Sequence 284592, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; SEQ ID NO 207
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-207

Query Match 89.7%; Score 35; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 7 EHDGIN 12

RESULT 7
US-10-424-599-170453
; Sequence 170453, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170453
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(131)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_124935C.1.pep
US-10-424-599-170453

Query Match 89.7%; Score 35; DB 12; Length 131;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 106 EHDGIN 111

RESULT 8
US-10-424-599-284592
; Sequence 284592, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284592
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99011C.1.pep
US-10-424-599-284592

Query Match 84.6%; Score 33; DB 12; Length 76;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
Db 54 EHDGLN 59

RESULT 9
US-10-083-357-1105
; Sequence 1105, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Qiaodong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REFERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 1105
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-1105

Query Match 82.1%; Score 32; DB 14; Length 17;
Best Local Similarity 71.4%; Pred. No. 9.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
Db 5 LSHDGLN 11

RESULT 10
US-09-270-983-4
; Sequence 4, Application US/09270983
; Publication No. US20020132327A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: HAY, Bruce A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING PROTEASES, PROTEASE TARGET SITES AND REGULATING PROTEASE ACTIVITY IN LIVING CELLS
; FILE REFERENCE: CIT1130-1
; CURRENT APPLICATION NUMBER: US/09/270,983
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/078,721
; PRIOR FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Product Synthesis, such as solid phase synthesis
US-09-270-983-4

Query Match 79.5%; Score 31; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGI 6
Db 11 IEHDGI 16

RESULT 11
US-10-424-599-234026
; Sequence 234026, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 234026
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_5334C.1.pep
US-10-424-599-234026

Query Match 79.5%; Score 31; DB 12; Length 66;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
Db 23 LEHQGLN 29

RESULT 12
US-09-747-287-203
; Sequence 203, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24892
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc.feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-203

Query Match 76.9%; Score 30; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
 |||||
 Db 8 HDGIN 12

RESULT 13
 US-09-874-350A-169
 ; Sequence 169, Application US/09874350A
 ; Publication No. US2004009626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oncoimmun, Inc.
 ; APPLICANT: Komoriya, Akira
 ; APPLICANT: Packard, Beverly
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
 ; FILE REFERENCE: 300-903840US
 ; CURRENT APPLICATION NUMBER: US/09/874,350A
 ; CURRENT FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: PCT/US98/00300
 ; PRIOR FILING DATE: 1998-02-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/24882
 ; PRIOR FILING DATE: 2000-09-11
 ; PRIOR APPLICATION NUMBER: US 09/394,019
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 08/802,981
 ; PRIOR FILING DATE: 1997-02-20
 ; NUMBER OF SEQ ID NOS: 221
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 169
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide substrate
 ; NAME/KEY: MOD.RES
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: K is blocked with Fmoc
 ; NAME/KEY: MOD.RES
 ; LOCATION: (14)..(14)
 ; OTHER INFORMATION: X is epsilon-aminocaproic acid
 ; NAME/KEY: MOD.RES
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: X is epsilon aminocaproic acid
 US-09-874-350A-169

Query Match 76.9%; Score 30; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
 |||||
 Db 8 HDGIN 12

RESULT 14
 US-10-424-599-210542
 ; Sequence 210542, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 210542
 ; LENGTH: 55
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32146C.1.pep
 US-10-424-599-210542

Query Match 76.9%; Score 30; DB 12; Length 55;
 Best Local Similarity 57.1%; Pred. No. 86;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
 :|||:
 Db 19 ISHDGIN 25

RESULT 15
 US-10-424-599-160368
 ; Sequence 160368, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 160368
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(70)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_115830C.1.pep
 US-10-424-599-160368

Query Match 76.9%; Score 30; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
 |||||
 Db 19 HDGIN 23

RESULT 16
 US-10-424-599-221259
 ; Sequence 221259, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 221259
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:

```
; NAME/KEY: unsure
; LOCATION: (1)..(121)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41827C.1.pep
US-10-424-599-221259

Query Match      76.9%; Score 30; DB 12; Length 121;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHDSIN 7
Db 77 MSHDGLN 83

RESULT 17
US-10-425-114-70959
; Sequence 70959, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70959
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMNO17238F01_FLI.pep
US-10-425-114-70959

Query Match      76.9%; Score 30; DB 12; Length 128;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHDSIN 7
Db 16 LHEGGIN 22

RESULT 18
US-09-947-387-73
; Sequence 73, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecul
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
```

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; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-73

Query Match      74.4%; Score 29; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDSIN 5
Db 1 LEHDSIN 5

RESULT 19
US-09-747-287-200
; Sequence 200, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc.feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287-200

Query Match      74.4%; Score 29; DB 12; Length 18;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHDSIN 7
Db 6 LETDGIN 12

RESULT 20
US-09-874-350A-166
; Sequence 166, Application US/09874350A
; Publication No. US2004009626A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
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\mathcal{L}_2^2 on $\mathcal{H}_0^1(\Omega) \times \mathcal{H}_0^1(\Omega)$

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; TITLE OF INVENTION:  AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 166
; LENGTH: 18
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon aminocaproic acid
; US-09-874-350A-166
;
; Query Match 74.4%; Score 29; DB 12; Length 18;
; Best Local Similarity 85.7%; Pred. No. 41;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; 1 LEHDGIN 7
;

```

```

RESULT 21
US-09-853-079-215
; Sequence 215, Application US/09853079
; Publication No. US20030109689A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Homer, Mary
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
; FILE REFERENCE: 210121.426C11
; CURRENT APPLICATION NUMBER: US/09/853,079
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 215
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Babesia microti
US-09-853-079-215

Query Match          74.4%; Score 29; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 EHDGIN 7
DB      6 EHDNIN 11

```

```
Publication No. US20040031072A1
GENERAL INFORMATION: Thomas J
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165583
LENGTH: 98
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(98)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_120537C.1.pep
US-10-424-599-165583

Query Match 74.4%; Score 29; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
DB 80 LEHDG 84

RESULT 25
US-10-424-599-203990
Sequence 203990, Application US/10424599
Publication No. US30040031072A1
GENERAL INFORMATION: Thomas J
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203990
LENGTH: 101
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_2622C.1.pep
US-10-424-599-203990

Query Match 74.4%; Score 29; DB 12; Length 101;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 7
DB 55 EHDG 60

RESULT 26
US-10-369-493-11679
Sequence 11679, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14258
LENGTH: 127
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14258

Query Match 74.4%; Score 29; DB 15; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
DB 93 LEHDG 97

RESULT 27
US-10-369-493-14258
Sequence 14258, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14258
LENGTH: 127
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14258

Query Match 74.4%; Score 29; DB 15; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
DB 93 LEHDG 97

RESULT 28
US-10-369-493-14694
Sequence 14694, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
```

; PRIOR APPLICATION NUMBER: US 60/360,039
; FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14694
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14694

Query Match 74.4%; Score 29; DB 15; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
| | | | |
Db 93 LEHDG 97

RESULT 29
US-10-424-599-147562
; Sequence 147562, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 147562
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(132)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104267C.1.pep
US-10-424-599-147562

Query Match 74.4%; Score 29; DB 12; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
| | | | |
Db 31 EHDGI 35

RESULT 30
US-10-198-070-26
; Sequence 26, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMELL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-26

Query Match 74.4%; Score 29; DB 14; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
| | | | |
Db 109 LQHQGVN 115

RESULT 31
US-10-422-571-19
; Sequence 19, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20082.00
; CURRENT APPLICATION NUMBER: US/10/422,571
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-19

Query Match 74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
| | | | |
Db 109 LQHQGVN 115

RESULT 32
US-10-422-571-29
; Sequence 29, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20082.00
; CURRENT APPLICATION NUMBER: US/10/422,571
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306

```
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-29

Query Match      74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHDCIN 7
Db      109 LQHGVN 115

RESULT 33
US-10-422-571-38
; Sequence 38, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-38

Query Match      74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHDCIN 7
Db      109 LQHGVN 115

RESULT 34
US-10-422-571-39
; Sequence 39, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00

; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-29

Query Match      74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHDCIN 7
Db      109 LQHGVN 115

RESULT 35
US-10-422-571-89
; Sequence 89, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-89

Query Match      74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHDCIN 7
Db      109 LQHGVN 115

RESULT 36
US-10-422-571-126
; Sequence 126, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
```

; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00
; CURRENT APPLICATION NUMBER: US/10/422,571
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-126

Query Match 74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHGDGIN 7
|:|:|:
Db 109 LQHQGVN 115

RESULT 37
US-10-422-571-130
; Sequence 130, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00
; CURRENT APPLICATION NUMBER: US/10/422,571
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-130

Query Match 74.4%; Score 29; DB 16; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHGDGIN 7
|:|:|:
Db 109 LQHQGVN 115

RESULT 38
US-10-221-278-647
; Sequence 647, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278

; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 647
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-647

Query Match 74.4%; Score 29; DB 12; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGI 6
|:|:|:
Db 63 EHDGI 67

RESULT 39
US-10-291-172-647
; Sequence 647, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 647
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-647

Query Match 74.4%; Score 29; DB 15; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGI 6
|:|:|:
Db 63 EHDGI 67

RESULT 40
US-10-424-599-262285
; Sequence 262285, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

```
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 262285
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_78865C.1.pep
US-10-424-599-262285

Query Match      71.8%; Score 28; DB 12; Length 49;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 EHDGIN 7
      |||
Db      28 EHGVN 33

RESULT 41
US-09-864-408A-116
; Sequence 116, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-116

Query Match      71.8%; Score 28; DB 11; Length 52;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 HDGIN 7
      |||
Db      32 HDGLN 36

RESULT 42
US-10-424-599-208279
; Sequence 208279, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208279
; LENGTH: 55

; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36300C.1.pep
US-10-424-599-208279

Query Match      71.8%; Score 28; DB 12; Length 55;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHDGIN 7
      :|||
Db      46 MQHGIN 52

RESULT 43
US-10-424-599-222247
; Sequence 222247, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 222247
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_42718C.1.pep
US-10-424-599-222247

Query Match      71.8%; Score 28; DB 12; Length 55;
Best Local Similarity 65.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEHDGI 6
      :|||
Db      38 LQHDGL 43

RESULT 44
US-10-424-599-215145
; Sequence 215145, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215145
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36300C.1.pep
US-10-424-599-215145

Query Match      71.8%; Score 28; DB 12; Length 68;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


QY 1 LEHDCI 6
Db 34 LSHDCI 39

RESULT 45

US-10-424-599-216092
; Sequence 216092, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216092
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37160C.1.pep
US-10-424-599-216092

Query Match 71.8%; Score 28; DB 12; Length 70;
Best Local Similarity 66.7%; Fred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
Db 35 EHDGLD 40

Search completed: June 15, 2004, 12:27:25
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 12:22:52 ; Search time 21 Seconds
(without alignments)
32.064 Million cell updates/sec

Title: US-09-394-019C-212

Perfect score: 39

Sequence: 1 LEHDGIN 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 293366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 72835

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	82.1	128	2 G72579	hypothetical prote
2	31	79.5	61	1 UPECX	D-Xylose uptake pr
3	30	76.9	80	2 H82194	conserved hypothet
4	30	76.9	114	2 G37938	hypothetical prote
5	29	74.4	64	2 S20961	keratinocyte growt
6	29	74.4	146	2 F90337	hypothetical prote
7	28	71.8	44	2 B46078	POU protein Emb, f
8	28	71.8	118	2 G64544	hypothetical prote
9	28	71.8	128	2 F71954	hypothetical prote
10	28	71.8	128	1 ERAD42	early E3s 14K prot
11	28	71.8	148	2 E95886	probable sugar-pho
12	27	69.2	70	2 T12911	hypothetical prote
13	27	69.2	76	2 T29085	hypothetical prote
14	27	69.2	114	2 B37938	hypothetical prote
15	27	69.2	115	2 T20983	hypothetical prote
16	27	69.2	125	2 F95121	conserved domain p
17	27	69.2	140	2 A48552	protein US420 - in
18	27	69.2	145	2 T16039	hypothetical prote
19	27	69.2	145	2 F73328	hypothetical prote
20	27	69.2	150	2 B97991	hypothetical prote
21	27	69.2	150	2 D81356	methyalted-DNA-[pr
22	26	66.7	58	2 A11911	30S ribosomal prot
23	26	66.7	83	2 H86911	hypothetical prote
24	26	66.7	88	2 A52845	conserved hypothet
25	26	66.7	93	2 H82607	conserved hypothet
26	26	66.7	97	2 A82059	hypothetical prote
27	26	66.7	98	2 T139650	superoxide dismuta
28	26	66.7	98	2 S78727	protein YLL018C-a
29	26	66.7	100	2 A31201	GII-related finger

RESULT 1

G72579

hypothetical protein APE1919 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C;Accession: G72579

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-Do, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: G72579

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <RAW>

A;Cross-references: DDBJ:AP000062; NID:G5105244; PIDN:BAA80924.1; PID:d1044710; PID:G510

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE1919

Query Match 82.1%; Score 32; DB 2; Length 128;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7

Db 116 LSHDGIN 122

RESULT 2

UPECX

D-Xylose uptake protein - Escherichia coli

C;Species: Escherichia coli

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999

C;Accession: A24334

R;Kurose, N.; Watanabe, K.; Kimura, A.

Nucleic Acids Res. 14, 7115-7123, 1986

A;Title: Nucleotide sequence of the gene responsible for D-xylose uptake in Escherichia

A;Reference number: A24334; MUID:87016348; PMID:3532033

A;Accession: A24334

A;Molecule type: DNA

A;Residues: 1-61 <KUR>

A;Cross-references: GB:X04387; NID:943317; PIDN:CAA27976.1; PID:G43318

C;Comment: This protein enables E. coli mutants to recover from a decrease in D-xylose ut

C;Genetics:

A;Map position: 80 min

C;Superfamily: D-xylose uptake protein

C;Keywords: xylose transport

Query Match 79.5%; Score 31; DB 1; Length 61;

Best Local Similarity 71.4%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|:|||||
Db 36 LQHDGIG 42

RESULT 3
H82194
conserved hypothetical protein VC1487 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82194
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.; Hlavinka, M.D.; Vanhatter, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82194
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-80 <HEI>
A:Cross-references: GB:AE004226; GB:AE003852; NID:99655979; PIDN:AAF94642.1; GSPDB:GN001194
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Map position: 1

Query Match 76.9%; Score 30; DB 2; Length 80;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|:|||||
Db 71 LKHNGIN 77

RESULT 4
G97938
hypothetical protein glnQ-truncation [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: G97938
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eick, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: G97938
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99339.1; PID:gl5458110; GSPDB:GN00174
C:Genetics:
A:Gene: glnQ-truncation

Query Match 76.9%; Score 30; DB 2; Length 114;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|:|||||
Db 47 LAHDGMN 53

RESULT 5
S20961
keratinocyte growth factor receptor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C:Accession: S20961

R:Yayon, A.; Zimmer, Y.; Guo-Hong, S.; Avivi, A.; Yarden, Y.; Givol, D.
EMBO J. 11, 1885-1890, 1992
A:Title: A confined variable region confers ligand specificity on fibroblast growth factor receptor
A:Reference number: S20961; MUID:92258398; PMID:1316275
A:Accession: S20961
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-64 <YAY>
C:Keywords: growth factor receptor

Query Match 74.4%; Score 29; DB 2; Length 64;
Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|:|||||
Db 1 LKHSGIN 7

RESULT 6
F90337
hypothetical protein SSO1764 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: F90337
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan, Y.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90337
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <KUR>
A:Cross-references: GB:AE006641; NID:gi3815007; PIDN:AAK41957.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1764

Query Match 74.4%; Score 29; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|||||
Db 101 LEHDG 105

RESULT 7
B46078
POU protein Emb. form c7 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 15-Oct-1999
C:Accession: B46078
R:Okamoto, K.; Wakamiya, M.; Noji, S.; Koyama, E.; Taniguchi, S.; Takemura, R.; Copeland, J. Biol. Chem. 268, 7449-7457, 1993
A:Title: A novel class of murine POU gene predominantly expressed in central nervous system
A:Reference number: A46078; MUID:93216691; PMID:8463278
A:Accession: B46078
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-44 <OKA>
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 71.8%; Score 28; DB 2; Length 44;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|:|||||
Db 26 LQHDGIN 32

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69925
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-70 <KUN>
A;Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13912.1; PID:el185492;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yorZ

Query Match 69.2%; Score 27; DB 2; Length 70;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
Db 57 LEHGLN 63

RESULT 13
T29085
hypothetical protein SC12.36 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T29085
R;Redenbach, M.; Kiese, H.M.; Denapate, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
Mol. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
A;Reference number: 220556; MUID:97000351; PMID:8843436
A;Accession: T29085
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-76 <RED>
A;Cross-references: EMBL:AL031124; NID:ei312893; PID:ei312929; PIDN:CAA20003.1
C;Genetics:
A;Note: SC12.36

Query Match 69.2%; Score 27; DB 2; Length 76;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDG 5
Db 1 MEHDG 5

RESULT 14
B83798
hypothetical protein BH1186 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B83798
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <STO>
A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA04905.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1186

Query Match 69.2%; Score 27; DB 2; Length 114;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGI 6
Db 50 MKHDGI 55

RESULT 15
T20983
hypothetical protein F15D4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20983
R;Smye, R.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19354
A;Accession: T20983
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-115 <WIL>
A;Cross-references: EMBL:Z80344; PIDN:CAB02489.1; GSPDB:GN00020; CESP:F15D4.6
A;Experimental source: clone F15D4
C;Genetics:
A;Gene: CESP:F15D4.6
A;Map position: 2
A;Introns: 41/2; 82/1

Query Match 69.2%; Score 27; DB 2; Length 115;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
Db 63 LENDGIN 69

RESULT 16
F95121
conserved domain protein SP1053 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95121
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95121
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75167.1; PID:g14972527; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1053

Query Match 69.2%; Score 27; DB 2; Length 125;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
Db 77 MESDGIN 83

RESULT 17
A48552
protein US420 - infectious laryngotracheitis virus
C;Species: infectious laryngotracheitis virus

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 08-Oct-1999
 C/Accession: A48552
 R/Sakaguchi, M.; Urakawa, T.; Hirayama, Y.; Miki, N.; Yamamoto, M.; Hirai, K.
 Virus Genes 6, 365-378, 1992
 A>Title: Sequence determination and Genetic content of an 8.9-kb restriction fragment in
 A/Reference number: A48552; MUID:93118245; PMID:1282282
 A/Accession: A48552
 A>Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-140 <SAK>
 A/Cross-references: GB:M80595; NID:g291557; PIDN:AAB59889.1; PID:g291558
 A/Note: sequence extracted from NCBI backbone (NCBIN:121622, NCBIPI:121623)
 C:Superfamily: infectious laryngotracheitis virus protein US420

Query Match 69.2%; Score 27; DB 2; Length 140;
 Best Local Similarity 71.4%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
 |::|:
 Db 35 LLEHGIN 41

RESULT 18
 Ti6039
 hypothetical protein F12A10.5 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Dec-1999
 C/Accession: Ti6039
 R/Geisel, C.
 submitted to the EMBL Data Library, June 1995
 A/Description: The sequence of C. elegans cosmid F12A10.
 A/Reference number: Z18451
 A/Accession: Ti6039
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-145 <GEI>
 A/Cross-references: EMBL:U28731; NID:G861241; PID:G861246; PIDN:AAA68298.1; CBSP:F12A10.
 A/Experimental source: strain Bristol N2
 C/Genetics:
 A/Gene: CBSP:F12A10.5
 A/Introns: 30/3; 56/1; 87/3; 137/1
 C:Superfamily: calmodulin; calmodulin repeat homology
 C/Keywords: EF hand

Query Match 69.2%; Score 27; DB 2; Length 145;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGDGI 6
 |::|:
 Db 127 LDHGDG 132

RESULT 19
 F97328
 hypothetical protein CAC3491 [imported] - Clostridium acetobutylicum
 C/Species: Clostridium acetobutylicum
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C/Accession: F97328
 R/Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: F97328
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-145 <KUR>
 A/Cross-references: GB:AE001437; PIDN:AAK81417.1; PID:g15026582; GSPDB:GN00168
 A/Experimental source: Clostridium acetobutylicum ATCC824
 C/Genetics:
 A/Gene: CAC3491

Query Match 69.2%; Score 27; DB 2; Length 145;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDDGI 6
 |::|:
 Db 39 LKHDDGL 44

RESULT 20
 B97991
 hypothetical protein spr0954 [imported] - Streptococcus pneumoniae (strain R6)
 C/Species: Streptococcus pneumoniae
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C/Accession: B97991
 R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; R
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A/Reference number: A97872; MUID:21429245; PMID:11544234
 A/Accession: B97991
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-150 <KUR>
 A/Cross-references: GB:AE007317; PIDN:AAK99758.1; PID:g15458564; GSPDB:GN00174
 C/Genetics:
 A/Gene: spr0954

Query Match 69.2%; Score 27; DB 2; Length 150;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDDGIN 7
 |::|:
 Db 102 MESDGVN 108

RESULT 21
 D81356
 methylated-DNA-[protein]-cysteine S-methyltransferase (EC 2.1.1.63) Cj0836 [imported] -
 C/Species: Campylobacter jejuni
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C/Accession: D81356
 R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrall
 Nature 403, 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A/Reference number: A81250; MUID:20150912; PMID:10688204
 A/Accession: D81356
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-150 <PAR>
 A/Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73101.1; PID:g696828
 A/Experimental source: serotype O2, strain NCTC 11168
 C/Genetics:
 A/Gene: OGT; Cj0836
 C/Keywords: methyltransferase

Query Match 69.2%; Score 27; DB 2; Length 150;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDDGIN 7
 |::|:
 Db 142 LENEQVN 148

RESULT 22
 A11911
 30S ribosomal protein s21 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AII1911
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A;Reference number: AB1807; UID:21595285; PMID:11759840
A;Accession: AII1911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-58 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72800.1; PID:g17130188; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 66.7%; Score 26; DB 2; Length 58;
Best Local Similarity 66.7%; Pred.No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
|||:
Db 8 EHEDGID 13

RESULT 23
H86911
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H86911
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hooley, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, R.; Kramarova, E.; Liao, S.; McAdam, K.W.J.; Mouton, R.; Parkhill, J.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Whittam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Whittam, M.A.; Rutherford, K.M.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; UID:21128732; PMID:11234002
A;Accession: H86911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <STO>
A;Cross-references: GB:AL450380; NID:g13092434; PIDN:CAC29532.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML0024

Query Match 66.7%; Score 26; DB 2; Length 83;
Best Local Similarity 50.0%; Pred.No. 1.5e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
|||:
Db 26 DHGDVD 31

RESULT 24
AH2845
conserved hypothetical protein Atu193 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2845
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; UID:21608550; PMID:11743193
A;Accession: AH2845

A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2059
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAF73723.1; PID:gl7131115; GSPDB:GN00179
A;Experimental source: strain POC 7120
C;Genetics:
A;Gene: asl2024

Query Match 66.7%; Score 26; DB 2; Length 97;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDCIN 7
||| :|||
Db 36 LEKEGIN 42

RESULT 27
I39650
superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Actinobacillus pleuropneumoniae (fragments)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 16-Aug-1996 #sequence revision 05-Mar-1999 #text_change 20-Jun-2000
A;Accession: I39650; S22815; S22161
R;Kroll, J.S.; Langford, P.R.; Wilks, K.E.; Keil, A.D.
Microbiology 141, 2271-2279, 1995
A;Title: Bacterial [Cu,Zn]-superoxide dismutase: Phylogenetically distinct from the euka
A;Reference number: I39485; MUID:96118708; PMID:7496539
A;Accession: I39650
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-87 <KRO>
A;Cross-references: EMBL:X83123; NID:gl019747; PIDN:CAA58204.1; PID:gl019748
R;Loynds, B.M.; Langford, P.R.; Kroll, J.S.
Nucleic Acids Res. 20, 615, 1992
A;Title: recF in Actinobacillus pleuropneumoniae.
A;Reference number: S22813; MUID:92158680; PMID:1741300
A;Accession: S22815
A;Molecule type: DNA
A;Residues: 88-98 <LOY>
A;Cross-references: EMBL:X63626; NID:g38951; PIDN:CAA45174.1; PID:g1333704
A;Note: This sequence was submitted to the EMBL Data Library, December 1991
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
C;Genetics:
A;Gene: sodC
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Cu-Zn)
C;Keywords: copper; metalloprotein; oxidoreductase; zinc
F:18,27,36,39/Binding site: zinc (His, His, His, Asp) #status predicted
F:91/Active site: Arg #status predicted

Query Match 66.7%; Score 26; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
:||||
Db 45 VEHDG 49

RESULT 28
S78727
protein YLL018c-a - Yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 15-Jan-1999 #sequence revision 15-Jan-1999 #text_change 15-Jan-1999
A;Accession: S78727
R;Goffeau, A.; Fumelle, B.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64761
A;Accession: S78727
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-98 <GOF>
A;Cross-references: EMBL:Z73125; MIPS:YLL018c-a
A;Experimental source: strain S288C
C;Genetics:
A;Map position: 12L

Query Match 66.7%; Score 26; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
:||||
Db 24 LDHDG 28

RESULT 29
A31201
GLI-related finger protein GLI2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 31-Dec-1993
A;Accession: A31201
R;Ruppert, J.M.; Kinzler, K.W.; Wong, A.J.; Bigner, S.H.; Kao, F.T.; Law, M.L.; Seauanez,
Mol. Cell. Biol. 8, 3104-3113, 1988
A;Title: The GLI-Kruppel family of human genes.
A;Reference number: A93103; MUID:89096896; PMID:2850480
A;Accession: A31201
A;Molecule type: DNA
A;Residues: 1-100 <RUP>
C;Genetics:
A;Introns: 50/2
C;Superfamily: gli transforming protein
C;Keywords: DNA binding; zinc finger

Query Match 66.7%; Score 26; DB 2; Length 100;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EHDGIN 7
||| :|||
Db 75 EHEGON 80

RESULT 30
A97623
hypothetical protein AGR_C3987 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: A97623
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87938.1; PID:gl5157340; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C3987
A;Map position: circular chromosome

Query Match 66.7%; Score 26; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
:||||
Db 22 VEHDG 26

RESULT 31

H86483
probable 60S ribosomal protein L30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: H86483
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86483
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <STO>
A:CROSS-references: GB:AE005172; NID:gl0645486; PIDN:AAG21599.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: rat ribosomal protein L30

Query Match	66.7%	Score 26;	DB 2;	Length 112;
Best Local Similarity	80.0%	Pred. No. 2.5e+02;		
Matches	4;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;

QY 3 HDGIN 7
|:|:|
DB 11 HEGIN 15

RESULT 32
AB2636
conserved hypothetical protein Atu0485 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AB2636
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:111743193
A:Accession: AB2636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KUR>
A:CROSS-references: GB:AE008688; PIDN:AAL41504.1; PID:gl7738832; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0485
A:Map position: circular chromosome
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2705c

Query Match	66.7%	Score 26;	DB 2;	Length 117;
Best Local Similarity	80.0%	Pred. No. 2.7e+02;		
Matches	4;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|:|
DB 105 LDHDG 109

RESULT 33
C95877
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: C95877
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95877
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-119 <KUR>
A:CROSS-references: GB:ALU591985; PIDN:CAC48683.1; PID:gl5140155; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pla, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20293
A:Genome: plasmid

Query Match	66.7%	Score 26;	DB 2;	Length 119;
Best Local Similarity	80.0%	Pred. No. 2.7e+02;		
Matches	4;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|:|
DB 9 VEHDG 13

RESULT 34
D87499
hypothetical protein CC2017 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87499
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87499
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <STO>
A:CROSS-references: GB:AE005673; NID:gl3423490; PIDN:AAK23992.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2017

Query Match	66.7%	Score 26;	DB 2;	Length 130;
Best Local Similarity	80.0%	Pred. No. 3e+02;		
Matches	4;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;

QY 1 LEHDG 5
|:|:|
DB 68 LDHDG 72

RESULT 35
T00002
peps protein - Acidianus ambivalens plasmid pDL10
C:Species: Acidianus ambivalens
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 20-Jun-2000
C:Accession: T00002
R:Kletzin, A.
submitted to the EMBL Data Library, January 1998
A:Description: The plasmid pDL10 from the extremely thermophilic archaeon Acidianus ambi
A:Reference number: Z14035
A:Accession: T00002

A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-135 <KLE>
A:Cross-references: EMBL:AJ225333; PIDN:CAA12519.1
A:Experimental source: strain Le110
C:Genetics:
A:Gene: pepG
A:Genome: plasmid pDL10
C:Superfamily: Acidianus ambivalens plasmid pDL10 pepG protein

Query Match 66.7%; Score 26; DB 2; Length 135;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
|||
DB 39 LERDGIS 45

RESULT 36
C49276
lek protein - Ectromelia virus
C:Species: Ectromelia virus
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
C:Accession: C49276
R:Senkevich, T.G.; Koonin, E.V.; Buller, R.M.L.
Virology 198, 118-128, 1994
A:Title: A poxvirus protein with a RING zinc finger motif is of crucial importance for
A:Reference number: A49276; MUID:94082441; PMID:8259647
A:Accession: C49276
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <SEN>
A:Cross-references: GB:U01161; NID:g397978; PIDN:AAAL6259.1; PID:g397981
C:Genetics:
A:Gene: p16

Query Match 66.7%; Score 26; DB 2; Length 138;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 LEH--DGIN 7
|||
DB 68 IEHLGDGIN 75

RESULT 37
T17493
citrate utilization determinant homolog A3R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T17493; T18191
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17493
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-141 <GRA>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAAC96371.1
A:Experimental source: specific host Chlorella strain NC64A
A:Accession: T18191
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-141 <GR2>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAAC96990.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Gene: A3R
A>Note: A689L

Query Match 66.7%; Score 26; DB 2; Length 141;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDI 6
|||
DB 85 LNHDL 90

RESULT 38
A54492
hemoglobin beta-II chain, larval - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 04-Mar-2000
C:Accession: A54492; A24119
R:Meyerhof, W.; Koester, M.; Stalder, J.; Weber, R.; Knoechel, W.
Mol Biol Rep. 11, 155-161, 1986
A:Title: Sequence analysis of the larval beta-II-globin gene of Xenopus laevis.
A:Reference number: A54492; MUID:87014375; PMID:3020391
A:Accession: A54492
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <MEY>
A:Cross-references: GB:M21411; NID:g213961; PIDN:AAA49653.1; PID:g213962
R:Knoechel, W.; Meyerhof, W.; Stalder, J.; Weber, R.
Nucleic Acids Res. 13, 7899-7908, 1985
A:Title: Comparative nucleotide sequence analysis of two types of larval beta-globin mRNA
A:Reference number: A24119; MUID:86067205; PMID:2999708
A:Accession: A24119
A:Molecule type: mRNA
A:Residues: 2-147 <XNO>
A:Cross-references: GB:X03142; NID:g64575; PIDN:CAA26914.1; PID:g64576
A>Note: Initiator Met not shown
C:Genetics:
A:Introns: 31/2; 105/3
C:Superfamily: Globin; globin homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxygen carrier
F:4-147/Domain: globin homology <GLB>
F:64/Binding site: oxygen (His) (proximal axial ligand) #status predicted
F:93/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 66.7%; Score 26; DB 2; Length 147;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
|||
DB 21 VEHDG 25

RESULT 39
A69137
hypothetical protein MTH291 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A69137
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; H
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69137
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-148 <MTH>
A:Cross-references: GB:AE000814; GB:AE000666; NID:g2621334; PIDN:AA84797.1; PID:g262134
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH291
C:Superfamily: hypothetical protein MTH291

Query Match 66.7%; Score 26; DB 1; Length 148;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      2 EHDGI 6
Db      71 DHDGI 75

RESULT 40
C70763
hypothetical protein Rvi558 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: C70763
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:3829598; PMID:9634230
A:Accession: C70763
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-148 <COL>
A:Cross-references: GB:274020; GB:AL123456; NID:G3261584; PIDN:CAA98333.1; PID:G1403484
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rvi558

Query Match      66.7%; Score 26; DB 2; Length 148;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEHDG 5
Db      59 VEHDG 63

RESULT 41
A84358
hypothetical protein vng2081h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84358
R:NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabil
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A>Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: A84358
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <STO>
A:Cross-references: GB:AE004437; NID:G10581498; PIDN:AKG20229.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG2081H

Query Match      64.1%; Score 25; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EHDG 5
Db      33 BHDG 36

RESULT 42
H86661
hypothetical protein ycjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: H86661

R:Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86661
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <STO>
A:Cross-references: GB:AE005176; PID:G12723159; PIDN:AAK04394.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: YCjF

Query Match      64.1%; Score 25; DB 2; Length 66;
Best Local Similarity 86.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 EHDGIN 7
Db      17 EFDGYN 22

RESULT 43
T17015
metallothionein-like protein AMT2 - apple tree
C:Species: Malus domestica (apple tree)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17015
R:Reig, S.J.; Ross, G.S.
Physiol. Plantarum 100, 183-189, 1997
A>Title: Up-regulation of two cDNA clones encoding metallothionein-like proteins in app
A:Reference number: Z18652
A:Accession: T17015
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-66 <REI>
A:Cross-references: EMBL:U61974; NID:G1655852; PID:G1655853
C:Genetics:
A:Gene: AMT2
C:Keywords: metal binding

Query Match      64.1%; Score 25; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EHDG 5
Db      46 EHDG 49

RESULT 44
G82027
hypothetical protein NMA0321 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G82027
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: G82027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB83626.1; PID:G737907
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0321

Query Match      64.1%; Score 25; DB 2; Length 68;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 EHDGI 6
Db 21 KHDGI 25

RESULT 45

B90762
hypothetical protein ECs1066 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: B90762
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kunara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <RAY>
A;Cross-references: GB:BA000007; PIDN:BA834489.1; PID:gl3360526; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 050952
C;Genetics:
A;Gene: ECs1066

Query Match 64.1%; Score 25; DB 2; Length 72;
Best Local Similarity 100.0%; Pred.No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 5
Db 65 EHDG 68

Search completed: June 15, 2004, 12:25:54
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 12:22:52 ; Search time 11 Seconds
(without alignments)
33.136 Million cell updates/sec

Title: US-09-394-019c-212

Perfect score: 39

Sequence: 1 LEHDGIN 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 30433

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	79.5	61	1 XYL1 ECOLI	P05056 escherichia
2	29	74.4	98	1 CH10_BHRSE	O32605 ehrlichia s
3	29	74.4	130	1 DSRE_CHRYI	O87896 chromatin
4	28	71.8	128	1 E314_ADE02	P03249 human adeno
5	28	71.8	148	1 Y105_FOWPV	Q915B5 fowlpox vir
6	27	69.2	140	1 U420_HSVMG	Q05103 marek's dis
7	26	66.7	58	1 R21B_ANASP	Q8YKX5 arabidopsi
8	26	66.7	112	1 R130_ARATH	Q915A3 arabidopsi
9	26	66.7	146	1 HB22_XENLA	P02133 xenopus lae
10	26	66.7	148	1 YF58_MYCTU	Q10772 mycobacteri
11	25	64.1	65	1 MT3_MUSAC	Q40256 musa acumin
12	25	64.1	66	1 MT3_MALDO	O24059 malus domes
13	25	64.1	66	1 SCXL_ANDAU	P80950 androctonus
14	25	64.1	80	1 IFIC_PSINU	Q8WHY8 psilotom nu
15	25	64.1	91	1 XIP_HUMAN	O43504 homo sapien
16	25	64.1	122	1 SUPA_ECOLI	P77667 escherichia
17	25	64.1	127	1 CMGF_BACSU	P25958 bacillus su
18	25	64.1	128	1 GC5H_NEIMA	Q9JVP1 neisseria m
19	25	64.1	138	1 YL75_PYRAE	Q8AVQ3 pyrobaculum
20	25	64.1	140	1 GVPO_HALME	Q02240 halobacteri
21	25	64.1	142	1 NDK_ECOL6	Q8FF53 escherichia
22	25	64.1	142	1 NDK_ECOLI	P24233 escherichia
23	25	64.1	142	1 NDK_SALTY	Q8XFN4 salmoneilla
24	25	64.1	144	1 Y991_METUA	Q58398 methanococc
25	25	64.1	146	1 KLA2_ECOLI	P52603 escherichia
26	25	64.1	146	1 PPDD_ECOLI	P36647 escherichia
27	24	61.5	60	1 YH05_VACCV	P17356 vaccinia vi
28	24	61.5	63	1 YDIE_ECOLI	P40721 escherichia
29	24	61.5	69	1 Y082_BACAN	Q9SMV3 bacillus an
30	24	61.5	73	1 LGEN_SOVIN	P59761 bos taurus
31	24	61.5	74	1 Z123_HUMAN	P35273 homo sapien
32	24	61.5	86	1 RNPH_PSEST	P57111 pseudomonas
33	24	61.5	95	1 RL25_HAEIN	P45281 haemophilus

ALIGNMENTS

RESULT 1

```

XYLU_ECOLI
ID XYL1 ECOLI STANDARD; PRT; 61 AA.
AC P05056;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Very hypothetical xylu protein.
GN XYL1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=87016348; PubMed=3532033;
RA Kurose N., Watanabe K., Kimura A.;
RT "Nucleotide sequence of the gene responsible for D-xylose uptake in
RT Escherichia coli.";
RL Nucleic Acids Res. 14:7115-7123 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGI1655;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakada S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saico N., Sampei G., Satoh Y., Sivasundaram S.,
RA Tagami H., Takanashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113 (1997).
CC -!- CAUTION: This sequence, according to the EcoSeq database (K. Rudd)
CC is probably not a real protein; therefore this entry will probably
CC be deleted in future releases.
-----
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-----
DR EMBL; X04387; CAA27976.1; -
DR EMBL; D90866; BAA16222.1; -
DR F01; A24334; UFECCX.
KW Hypothetical protein.
SQ SEQUENCE 61 AA; 6305 MW; 398B704F1B7CA3CA CRC64;

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Query Match 79.5%; Score 31; DB 1; Length 61;
Best Local Similarity 71.4%; Pred. No. 5.2;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHNGIN 7
Db 36 LQHDG1S 42

RESULT 2
ID CH10_EHRSR STANDARD; PRT; 98 AA.
AC 032605;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 10 kDa chaperonin (Protein Cpn10) (groES protein).
GN GROS OR GROES.
OS Enrichia sennetsu.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Neorickettsia.
OX NCBI_TaxID=951;
RN SEQUENCE FROM N.A.
RP STRAIN=Japan;
RX MEDLINE=97359489; PubMed=9215585;
RA Zhang Y., Ohashi N., Lee E.H., Tamura A., Rikihisa Y.;
RT "Enrichia sennetsu groE operon and antigenic properties of the GroEL homolog.";
RL FEMS Immunol. Med. Microbiol. 18:39-46(1997).
CC -!- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses the ATPase activity of the latter.
CC -!- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By similarity).
CC -!- SIMILARITY: Belongs to the groES chaperonin family.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the groES chaperonin family.

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EMBL; U88092; AAB64089.1; -;
HSSP; P05380; 1AON.
DR HAMAP; MF 00580; -; 1.
DR InterPro; IPR001476; Chaprin_Cpn10.
DR Pfam; PF00166; cpn10; 1.
DR PRINTS; PR00297; CHAPERONIN10.
DR PRODom; PD000566; Chaprin_Cpn10; 1.
DR PROSITE; PS00681; CHAPERONINS_CPN10; FALSE_NEG.
KW Chaperone.
SQ SEQUENCE 98 AA; 10621 MW; 4E566F4E9D7A0CA8 CRC64;

Query Match 74.4%; Score 29; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHNGI 6
Db 76 VEHDGV 81

RESULT 3
ID DSRE_CHRVI STANDARD; PRT; 130 AA.
AC 087896;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Intracellular sulfur oxidation protein dsrE.
GN DSRE.
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochromatium.

OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / ATCC 17899 / DSM 180;
RX MEDLINE=98361034; PubMed=9695921;
RA Pott A.S., Dani C.;
RT "Sirohaem sulfite reductase and other proteins encoded by genes at the dsr locus of Chromatium vinosum are involved in the oxidation of intracellular sulfur.";
RL Microbiology 144:1881-1894(1998).
CC -!- FUNCTION: NOT KNOWN. COULD BE INVOLVED IN THE OXIDATION OF INTRACELLULAR SULFUR.
CC -!- SIMILARITY: Belongs to the UPF0163 (dsrE) family.

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EMBL; U84760; AAC35396.1; -;
DR HAMAP; MF 00390; -; 1.
DR InterPro; IPR003787; DsrE.
DR Pfam; PF02635; DsrE; 1.
SQ SEQUENCE 130 AA; 14588 MW; 1429B54A99211B94 CRC64;

Query Match 74.4%; Score 29; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
Db 41 HDGVN 45

RESULT 4
E314_ADE02
ID E314_ADE02 STANDARD; PRT; 128 AA.
AC F03249;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Early E3B 14 kDa protein.
OS Human adenovirus type 2, and
OS Human adenovirus type 6.
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515, 10534;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human adenovirus type 2;
RX MEDLINE=81198965; PubMed=6362722;
RA Heriase J., Galibert F.;
RT "Nucleotide sequence of the EcoRI E fragment of adenovirus 2 genome.";
RL Nucleic Acids Res. 9:1229-1240(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human adenovirus type 6;
RX Reichmann H., Schaarschmidt E., Gaisler B., Hausmann J., Ortman D., Bauer U., Flunker G., Seidel W.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=90156523; PubMed=2304142;
RA Horton T.H., Tollefson A.E., Wold W.S.M., Gooding L.R.;
RT "A protein serologically and functionally related to the group C E3 14,700-kilodalton protein is found in multiple adenovirus serotypes.";
RL J. Virol. 64:1250-1255(1990).
CC -!- FUNCTION: Protects virus-infected cells from TNF-induced cytotoxicity.
CC -!- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.

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CC -----
DR EMBL; J01917; ; NOT ANNOTATED_CDS.
DR EMBL; V16037; CA875954.1; -.
DR PIR; A03818; ERA042.
DR InterPro; IPR004985; Adeno_E3_153.
DR Pfam; PF03307; Adeno_E3_153; 1.
DR Early protein.
KW SEQUENCE 128 AA; 14738 MW; 09882D90B253F146 CRC64;
SQ
Query Match 71.8%; Score 28; DB 1; Length 128;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEHDGIN 7
DB 7 LELDGIN 13
RESULT 5
V105_FOWPV STANDARD; PRT; 148 AA.
AC Q9J5B5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein FFW105.
GN FFW105.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -!- SIMILARITY: BELONGS TO THE POXVIRUSES F15 FAMILY.
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CC -----
DR EMBL; AF198100; AAF44449.1; -.
DR InterPro; IPR007675; Pox_F15.
DR Pfam; PFO4596; Pox_F15; 1.
DR PRSF; PRSF015694; VAC_F15L; 1.
DR PRSF; PRSF015694; VAC_F15L; 1.
SQ SEQUENCE 148 AA; 17723 MW; 492B0CB93D6B02A CRC64;
Query Match 71.8%; Score 28; DB 1; Length 148;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGIN 7
DB 111 EHNGIN 116
RESULT 6
U420_HSVMG STANDARD; PRT; 140 AA.
ID U420_HSVMG
```

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AC Q05103;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 15.5 kDa protein.
GN U5420.
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=93118245; PubMed=1282282;
RA Sakaguchi M., Urakawa T., Hirayama Y., Miki N., Yamamoto M.,
RA Hirai K.;
RT "Sequence determination and genetic content of an 8.9-kb restriction
RT fragment in the short unique region and the internal inverted repeat
RT of Marek's disease virus type 1 DNA.";
RL Virus Genes 6:365-378(1992).
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CC -----
DR EMBL; M80595; AAB59889.1; -.
DR Hypothetical protein.
KW SEQUENCE 140 AA; 15496 MW; C3A73F42C3CA6545 CRC64;
Query Match 69.2%; Score 27; DB 1; Length 140;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEHDGIN 7
DB 35 LLHEGIN 41
RESULT 7
R21B_ANASP STANDARD; PRT; 58 AA.
ID R21B_ANASP
AC Q8YK5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 30S ribosomal protein S21.B.
GN RPS22 OR RPS21 OR ASR0843.
OS Anabaena sp. (Strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21595255; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -!- SIMILARITY: Belongs to the S21P family of ribosomal proteins.
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CC -----
DR EMBL; AF003583; BAB72800.1; -.
DR FIR; A11911; A11911.
DR HAMAP; MF_00358; -; 1.
DR InterPro; IPR001911; Ribosomal_S21.
DR Pfam; PF01165; Ribosomal_S21; 1.
DR PRINTS; PR00976; RIBOSOMALS21.
DR ProDom; PD005521; Ribosomal_S21; 1.
DR TIGRfam; TIGR00030; S21p; 1.
DR PROSITE; PS01181; RIBOSOMAL_S21; 1.
DR Ribosomal protein; Complete proteome.
DR KW SEQUENCE 58 AA; 6901 MW; 5BD5B286A93A9B4D CRC64;
SQ
Query Match 66.7%; Score 26; DB 1; Length 58;
Best Local Similarity 66.7%; Pred.No. 60;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGIN 7
DB 8 EHEGID 13
|||:
|||:

RESULT 8
RL30 ARATH STANDARD; PRT; 112 AA.
ID RL30 ARATH
AC Q9LGA3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 6CS ribosomal protein L30.
DE RPL30 OR A7G18740 OR MVE11.10.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euraids II; Brassicales; Brassicaceae; Arabidopsais.
OC NCBI_TaxID=3702;
CX [1]
SEQUENCE FROM N.A.
RN STRAIN=cv. Columbia;
RC MEDLINE=20277480; PubMed=10819329;
RX Sato S., Nakamura Y., Kaneo T., Katoh T., Asamizu E., Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 3. I.
RT Sequence features of the regions of 4,504,864 bp covered by sixty P1
RT and TAC clones.";
RL DNA Res. 7:131-135(2000).
CC -!- SIMILARITY: Belongs to the L30E family of ribosomal proteins.
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CC -----
DR EMBL; AB026554; BAB01800.1; -.
DR HSSP; P14120; ICN9.
DR InterPro; IPR000231; Ribosomal_L30E.
DR InterPro; IPR004038; Ribosomal_L7A.
DR Pfam; PF01248; Ribosomal_L7Ae; 1.
DR ProDom; PD004495; Ribosomal_L30e; 1.
DR PROSITE; PS00709; RIBOSOMAL_L30E_1; 1.
DR PROSITE; PS00993; RIBOSOMAL_L30E_2; 1.
DR Ribosomal protein.
KW SEQUENCE 112 AA; 12279 MW; B1B2286ED2CC0549 CRC64;
SQ
Query Match 66.7%; Score 26; DB 1; Length 112;
Best Local Similarity 80.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
DB 11 BEGIN 15
|||:
|||:

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein RV1558/MT1609/MD1584.
GN RV1558 OR MT1609 OR MTCV48.07C OR MB1584.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Hatt D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duttoy S., Gordin S., Lacroix C., Monsenpe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RA "The complete genome sequence of Mycobacterium bovis.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
RL [1]
RP -1- SIMILARITY: TO M.TUBERCULOSIS RV1261C.
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CC -----
CC EMBL; Z74020; CAA98333.1; -;
DR EMBL; AR007027; AAK45876.1; -;
DR EMBL; BX248339; CAD96251.1; -;
DR PIR; C70763; C70763.
DR TIGR; MT1609; -;
DR TubercuList; RV1558; -;
DR InterPro; IPR004378; Mtu_fam_11.
DR Pfam; PF04075; DUF385; 1.
DR TIGRFAMs; TIGR00026; Mtu_fam_11; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 148 AA; 16347 MW; A9F98E9039871938 CRC64;
Query Match 66.7%; Score 26; DB 1; Length 148;
Best Local Similarity 80.0%; Pred No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEHDG 5

Db 59 VEHDG 63
|||||
RESULT 11
MT3_MUSAC
ID MT3_MUSAC STANDARD; PRT; 65 AA.
AC Q40256;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Metallothionein-like protein type 3 (MT-3).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Grand nain;
RX MEDLINE=98002325; PubMed=9342866;
RA Clendennen S.K., May G.D.;
RT "Differential gene expression in ripening banana fruit.";
RL Plant Physiol. 115:463-469(1997).
CC -1- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -1- SIMILARITY: Belongs to the metallothionein superfamily; family 15.
CC -----
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CC -----
CC EMBL; U49044; BAB82615.1; -;
DR InterPro; IPR000347; Metallothion_15.
DR Pfam; PF01439; Metallothion_2; 1.
DR ProDom; PD001611; Metallothion_15; 1.
KW Metal-binding; Metal-thiolate cluster.
SQ SEQUENCE 65 AA; 6774 MW; F456C0568AB4B577 CRC64;
Query Match 64.1%; Score 25; DB 1; Length 65;
Best Local Similarity 100.0%; Pred No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDG 5
|||||
Db 45 EHDG 48
RESULT 12
MT3_MALDO
ID MT3_MALDO STANDARD; PRT; 66 AA.
AC O24059;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Metallothionein-like protein type 3 (MT-3).
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RA Reid S.J., Ross G.S.;
RT "Up-regulation of two cDNA clones encoding metallothionein-like
RT proteins in apple fruit during cool storage.";
RL Physiol. Plantarum 100:183-189(1997).
CC -1- FUNCTION: Metallothioneins have a high content of cysteine

CC residues that bind various heavy metals.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily; family 15.
CC -----
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CC -----
DR EMBL; U61974; AAC23698.1; --
DR PIR; T17015; T17015.
DR InterPro; IPR000347; Metallothion_15.
DR ProDom; PD001611; Metallothion_15; 1.
KW Metal-binding; Metal-thiolate cluster.
SQ SEQUENCE 66 AA; 6930 MW; BFCF793C36FC036E CRC64;

Query Match 64.1%; Score 25; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 5
Db 46 EHDG 49

RESULT 13
SCXL_ANDAU STANDARD; PRT; 66 AA.
AC P80950;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurotoxin-like protein STR1 (Anatoxin AaH STR1) (AaHSTR1).
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Eutherozoa; Buthidae; Androctonus.
OX NCBI_TaxID=6958;
RN [1]
RP SEQUENCE.
RC STRAIN=Hector; TISSUE=Venom;
RA Mansuete P., Hassani O., Cestele S., Loret E.P., van Dorselaer A.,
RA Rochat H., Sampieri F.;
RL Submitted (AUG-1997) to Swiss-Prot.
RN [2]
RP STRUCTURE BY NMR.
RC STRAIN=Hector.
RX MEDLINE=97433298; PubMed=9288938;
RA Blanc E., Hassani O., Meunier S., Mansuete P., Sampieri P.,
RA Rochat H., Darbon H.;
RT "1H-NMR-derived secondary structure and overall fold of a natural
anatoxin from the scorpion Androctonus australis hector";
RL Eur. J. Biochem. 247:1118-1126(1997).
CC -!- FUNCTION: This protein is not toxic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-
toxin subfamily.
DR HSP; P01484; 1AHO.
DR InterPro; IPR003614; Kntn1.
DR InterPro; IPR002061; Scorpion_toxinL.
DR Pfam; PF00537; toxin_3; 1.
DR ProDom; PD000908; Scorpion_toxinL; 1.
DR SMART; SM00505; Kntn1; 1.
FT DISULFID 13 64
FT DISULFID 17 40
FT DISULFID 26 45
FT DISULFID 30 47
SQ SEQUENCE 66 AA; 7641 MW; D1B6487C4E8467E3 CRC64;

Query Match 64.1%; Score 25; DB 1; Length 66;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HDGIN 7
Db 8 HDGTN 12

RESULT 14
IFIC_PSINU STANDARD; PRT; 80 AA.
ID IFIC_PSINU
AC Q8WHY8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Translation initiation factor IF-1, chloroplast.
GN INFA.
OS Psilotum nudum (Whisk fern).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Moniliformopses; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
OX NCBI_TaxID=3240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kinyoku;
RA Wakasugi T., Nishikawa A., Yamada K., Sugiyama M.;
RT "Complete nucleotide sequence of the chloroplast genome from a fern,
Psilotum nudum";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: No specific function has so far been attributed to this
initiation factor; however, it seems to stimulate more or less all
the activities of the other two initiation factors, IF-2 and IF-3.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the IF-1 family.
CC -!- SIMILARITY: Contains 1 S1-like domain.
CC -----
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CC -----
DR EMBL; AF004638; BAB84251.1; --
DR HAMAP; MF_00075; --; 1.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR003029; S1.
DR InterPro; IPR006196; S1_IP1.
DR InterPro; IPR004368; TIF_IP1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00008; infa; 1.
DR PROSITE; PS00832; S1_IP1_TYPE; 1.
KW Initiation factor; Protein biosynthesis; Chloroplast.
FT DOMAIN 1 72
FT DOMAIN 1 72
SQ SEQUENCE 80 AA; 9299 MW; CB632F174EACDB7D CRC64;

Query Match 64.1%; Score 25; DB 1; Length 80;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EHDGIN 7
Db 3 EHDLIN 8

RESULT 15
XIP_HUMAN STANDARD; PRT; 91 AA.
ID XIP_HUMAN
AC Q43504;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hepatitis B virus X interacting protein (HBX-interacting protein) (HBV)
DE X interacting protein).
GN HBXP OR XIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE=Liver.
RX MEDLINE=98139062; PubMed=9499022;
RA Melegari M., Scaglioni P.P., Wands J.R.;
RT "Cloning and characterization of a novel hepatitis B virus X binding
RT protein that inhibits viral replication.";
RL J. Virol. 72:1737-1743(1998).
CC -|- FUNCTION: Binds to hepatitis B virus (HBV) C-terminus and
CC down-regulating hepatitis B virus (HBV) replication.
CC -|- TISSUE SPECIFICITY: Highly expressed in skeletal and cardiac
CC muscle, followed by pancreas, kidney, liver, brain, placenta and
CC lung.
CC
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CC
CC -----
CC EMBL; AF029890; AAC52032.1; -;
CC Genew; HGNC:17955; HBXP.
DR GO; GO:0003800; F:antiviral response protein activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR GO; GO:0008166; P:viral replication; TAS.
FT MUTAGEN 12 12 T->A: NO CHANGE.
FT MUTAGEN 36 36 (TRUNCATED FORM OF HBX).
FT SEQUENCE 91 AA; 9614 MW; 01D9E762ABC63990 CRC64;
Query Match 64.1%; Score 25; DB 1; Length 91;
Best Local Similarity 80.0%; Pred. NO. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGI 6
DB 78 KHDGI 82
RESULT 16
SUFA_ECOLI
ID SUFA_ECOLI STANDARD; PRT; 122 AA.
AC P77667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sufa protein.
GN SUFA OR B1684.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-Xb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP GENE NAME.
RC STRAIN=K12 / MG1655;
RX MEDLINE=99255563; PubMed=10322040;
RA Patzer S.I., Hantke K.;
RT "Sufo is a Nifs-like protein, and Sufo is necessary for stability of
RT the 2Pe-2S Phup protein in Escherichia coli.";
RL J. Bacteriol. 181:3307-3309(1999).
CC -|- SIMILARITY: BELONGS TO THE HESB/YADR/YFHF FAMILY.
CC
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CC
CC -----
CC EMBL; AB000263; AAC74754.1; -;
CC EMBL; D90811; BAA15453.1; -;
CC EMBL; D90812; BAA15459.1; -;
CC PIR; D64926; D64926.
CC Ecogene; EGI1378; sufa.
DR InterPro; IPR000361; HESB_yadr_yfHF.
DR Pfam; PF01521; HESB-like; 1.
DR ProDom; PD002183; HESB_yadr_yfHF; 1.
DR TIGRFAMs; TIGR00049; TIGR00049; 1.
DR PROSITE; PS01152; HESB; 1.
KW Complete proteome.
SQ SEQUENCE 122 AA; 13300 MW; D26917F42B4B740B CRC64;
Query Match 64.1%; Score 25; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. NO. 2.3e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDG 5
DB 71 EHDG 74
RESULT 17
CMGF_BACSU
ID CMGF_BACSU STANDARD; PRT; 127 AA.
AC P25958; O32021.
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Comg operon protein 6.
GN COMGF OR COMG6 OR BSU24680.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90008773; PubMed=2507524;
RA Albano M., Breittling R., Dubnau D.A.;
RT "Nucleotide sequence and genetic organization of the Bacillus
RT subtilis comg operon.";
RL J. Bacteriol. 171:5386-5404(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;

RA MEDLINE=9804033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriello R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Goldlighty B.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presacco E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solido B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viarri A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
RN [3]
RN FUNCTION.
RP MEDLINE=98083053; PubMed=9422590;
RX Chung Y.S., Dubnau D.A.;
RA "All seven comG open reading frames are required for DNA binding
RT during transformation of competent Bacillus subtilis";
RL J. Bacteriol. 180:41-45(1998).
RN [4]
RN SUBCELLULAR LOCATION.
RP MEDLINE=98389321; PubMed=9732928;
RX Chung Y.S., Braid F., Dubnau D.A.;
RA "Cell surface localization and processing of the ComG proteins,
RT required for DNA binding during transformation of Bacillus subtilis";
RL Mol. Microbiol. 29:905-913(1998).
CC -!- FUNCTION: Required for transformation and DNA binding.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -----
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CC -----
CC EMBL; M29691; AAA83372.1; ALT_INIT.
DR EMBL; Z99116; CAB14399.1; --
DR PIR; G30338; G30338.
DR PIR; G69603; G69603.
DR Subtilist; BG10488; comGF.
KW Competence; Membrane; Complete proteome.
SQ SEQUENCE 127 AA; 14281 MW; 6598AA28873AD84F CRC64;
Query Match 64.1%; Score 25; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDG 5
DB 20 EHDG 23

RESULT 18
GCSH_NEIMA
ID_GCSH_NEIMA STANDARD; PRT; 128 AA.
AC Q9JVE1.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glycine cleavage system H protein.
DE GCVH OR NNA0759.
GN Neisseria meningitidis (serogroup A).
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham K., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491";
RL Nature 404:502-506(2000).
CC -!- FUNCTION: The glycine cleavage system catalyzes the degradation of
CC glycine. The H protein shuttles the methylamine group of glycine
CC from the P protein to the T protein (By similarity).
CC -!- COPACITOR: The H chain contains a covalently-bound lipoyl cofactor
CC (By similarity).
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L and H (By similarity).
CC -!- SIMILARITY: Belongs to the gcvH family.
CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.
CC -----
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CC -----
CC EMBL; AL162754; CAB84042.1; --
DR PIR; H81919; H81919.
DR HSSP; P16048; LHTP.
DR HAMAP; MF_00272; --; 1.
DR InterPro; IPR002930; GCV_H.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF01597; GCV_H; 1.
DR TIGRFAMs; TIGR00527; gcvH; 1.
DR PROSITE; PS00189; LIPOYL; 1.
KW Lipoyl; Complete proteome.
FT BINDING 66 66 LIPOYL (BY SIMILARITY).
SQ SEQUENCE 128 AA; 13640 MW; 065F4ED8189DC74 CRC64;
Query Match 64.1%; Score 25; DB 1; Length 128;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEHDGI 6
DB 20 LEEDGI 25

RESULT 19
YL75_PYRAE
ID_YL75_PYRAE STANDARD; PRT; 138 AA.
AC Q8ZVQ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
 DR Hypothetical UPF0217 protein PAE2175.
 DE PAF2175.
 GN Pyrobaculum aerophilum.
 OS Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX MEDLINE=21664397; PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 CC -!- SIMILARITY: Belongs to the UPF0217 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB009861; AAL64003.1; -.
 DR HAMAP; MF 00587; atypical; 1.
 DR InterPro; IPR007158; DUF358.
 DR Pfam; PF04013; DUF358; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 138 AA; 15818 MW; DB88C30BAC221619 CRC64;
 Query Match 64.1%; Score 25; DB 1; Length 138;
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGIN 7
 DB :|||:
 95 DHDGLS 100
 RESULT 20
 GVPO HALME STANDARD; PRT; 140 AA.
 ID GVPO HALME STANDARD; PRT; 140 AA.
 AC Q02240;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Gvpo protein.
 GN GVPO.
 OS Halobacterium mediterranei (Haloflex mediterranei).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Haloflex.
 OX NCBI_TaxID=2252;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1411;
 RX MEDLINE=93021102; PubMed=1404376;
 RA Englert C., Krueger K., Offner S., Pfeifer F.;
 RT "Three different but related gene clusters encoding gas vesicles in
 RT halophilic archaea";
 RL J. Mol. Biol. 227:586-592(1992).
 CC -----
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 CC -----
 CC EMBL; X64701; CAA45942.1; -.
 DR

PIR; S28113; S28113.
 DR InterPro; IPR008634; Gvpo.
 DR Pfam; PF05800; Gvpo; 1.
 KW Gas vesicle.
 SQ SEQUENCE 140 AA; 15306 MW; B97A2A43E3B56BP4 CRC64;
 Query Match 64.1%; Score 25; DB 1; Length 140;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDGIN 7
 DB :|||:
 11 HDGID 15
 RESULT 21
 NDK_ECOL6 STANDARD; PRT; 142 AA.
 ID NDK_ECOL6 STANDARD; PRT; 142 AA.
 AC Q8FF53;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)
 DE (Nucleoside-2-P kinase).
 GN NDK CR C3041.
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:HI / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 CC -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
 CC other than ATP.
 CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
 CC nucleoside triphosphate.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the NDK family.
 CC -----
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 CC -----
 CC EMBL; AB016764; AAN81491.1; -.
 DR HAMAP; MF 00451; -; 1.
 DR InterPro; IPR001564; NDK.
 DR Pfam; PF00334; NDK; 1.
 DR PRINTS; PR01243; NUOCPKINASE.
 DR PRODOM; PD001018; NDK; 1.
 DR SMART; SM00562; NDK; 1.
 DR PROSITE; PS00469; NDP_KINASES; 1.
 KW Transferase; Kinase; ATP-binding; Phosphorylation; Complete proteome.
 FT INIT MET 0 BY SIMILARITY.
 FT ACT_SITE 116 116 BY SIMILARITY.
 FT MOD_RES 118 118 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 120 120 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 142 AA; 15305 MW; DFB5C0D7A842379 CRC64;
 Query Match 64.1%; Score 25; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDG 5
|
|
|
|
52 EHDG 55

RESULT 22
NDK_ECOLI NDK_ECOLI
ID AC P24233; STANDARD; PRT; 142 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)
DE (Nucleoside-2-P kinase).
GN NDK OR B9518 OR Z3781 OR ECS3380 OR SF2564 OR S2736.
OS Escherichia coli.
OS Escherichia coli, O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334, 623;
[1] RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=K12;
RC MEDLINE=92039015; PubMed=1657712;
RX Hama H., Almaula N., Lerner C.G., Inouye S., Inouye M.;
RA "Nucleoside diphosphate kinase from Escherichia coli; its
RT overproduction and sequence comparison with eukaryotic enzymes.";
RL Gene 105:31-36(1991).
[2] RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=K12;
RC MEDLINE=97428617; PubMed=9278503;
RX Blattnner F.R.; Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RG Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
[3] RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=K12;
RC MEDLINE=97349980; PubMed=9205937;
RX Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubraman S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
[4] RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Rose D.J., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattnner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
[5] RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
[6] RN SEQUENCE OF 1-45.
RP SPECIES=E.coli;
RC MEDLINE=92362321; PubMed=1323446;
RX Ray N.B., Mathews C.K.;
RA "Nucleoside diphosphokinase: a functional link between intermediary
RT metabolism and nucleic acid synthesis";
RL Curr. Top. Cell. Regul. 33:343-357(1992).
[7] RN CHARACTERIZATION, AND PARTIAL SEQUENCE.
RP SPECIES=E.coli;
RC MEDLINE=95247689; PubMed=7730286;
RX Almaula N., Lu Q., Belgado J., Belkin S., Inouye M.;
RA "Nucleoside diphosphate kinase from Escherichia coli";
RL J. Bacteriol. 177:2524-2529(1995).
[8] RN SEQUENCE OF 1-11.
RP SPECIES=E.coli; STRAIN=K12 / W3110;
RC Frutiger S., Hughes G.J., Pasquali C., Hochstrasser D.F.;
RL Submitted (FEB-1996) to Swiss-Prot.
[9] RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RC MEDLINE=22727406; PubMed=12384590;
RX Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157";
RL Nucleic Acids Res. 30:4432-4441(2002).
[10] RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RC MEDLINE=22590274; PubMed=12704152;
RX Wei J., Goldberg M.B., Burland V., Vankatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattnner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T";
RL Infect. Immun. 71:2775-2786(2003).
CC -1- FUNCTION: Major role in the synthesis of nucleoside triphosphates
CC other than ATP
CC -1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
CC nucleoside triphosphate.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the NDK family.

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CC EMBL; X57555; CAA40780.1; -;
DR EMBL; AE000338; AAC75571.1; -;
DR EMBL; D90881; BAA16405.1; -;
DR EMBL; D90882; BAA16409.1; -;
DR EMBL; AE005481; AAG57628.1; -;
DR EMBL; AP002561; BAB36803.1; -;
DR EMBL; AE015272; AAN4064.1; -;
DR EMBL; AE016387; AAP17891.1; -;
DR PIR; D91051; D91051.

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DR PIR; H85895; H85895.
DR PIR; JH0495; JH0495.
DR HSP; P15266; INHK.
DR HSP; P24233; -.
DR SWISS-2DPAGE; P24233; COLI.
DR Ecogene; E010650; ndk.
DR HAMAP; MF_00451; -.
DR InterPro; IPR001564; NDK.
DR Pfam; PF00334; NDK; 1.
DR PRINTS; PR01243; NUCDPKINASE.
DR ProDom; PD001018; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Transferase; Kinase; ATP-binding; Phosphorylation; Complete proteome.
FT INIT MET 0
FT ACT SITE 116 116
FT MOD_RES 118 118 PHOSPHORYLATION.
FT MOD_RES 120 120 PHOSPHORYLATION.
SQ SEQUENCE 142 AA; 15332 MW; DFB7AC107A842364 CRC64;

Query Match 64.1%; Score 25; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 5
DB 52 EHDG 55

RESULT 23
NDK_SALTY STANDARD; PRT; 142 AA.
AC Q8XFN4,
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)
DE (Nucleoside-2-P kinase).
GN NDK OR STM2526 OR STY2771 OR T0330.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]_
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=1677609;
RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=1677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18."
J. Bacteriol. 185:2330-2337(2003).
FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP.
CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the NDK family.

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EMBL; AE008814; AAL21420.1; -.
EMBL; AL627275; CAD02729.1; -.
EMBL; AE016835; AAC068053.1; -.
StyGene; SG23232?; ndk.
HAMAP; MF_00451; -.
InterPro; IPR001564; NDK.
Pfam; PF00334; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP_KINASES; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
INIT_MET 0 BY SIMILARITY.
ACT_SITE 116 116 BY SIMILARITY.
SEQUENCE 142 AA; 15390 MW; C27B2B10BFF7F919 CRC64;

Query Match 64.1%; Score 25; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 5
DB 52 EHDG 55

RESULT 24
Y991_METJUA STANDARD; PRT; 144 AA.
AC Q58398;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0991.
GN MJ0991.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2651 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., FitzGerald L.M., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitts Gerald L.M., Tomb J.-F., Adams M.D., Reich C.I.,
RA Kervlavage A.R., Dougherty B.A., Tomb J.-F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Overbeek R., Kirkness E.F., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Sadow P.W., Hanna M.C.,
RA Utterback T.R., Kelley J.M., Hurst M.M., Kaine B.P., Borodovsky M.,
RA Cotton M.D., Roberts K.M., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

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RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii."
RL Science 273:1058-1073(1996).
CC -----
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CC -----
DR EMBL; U67541; AAB98996.1; -.
DR PIR; G64423; G64423.
DR TIGR; MJ0991; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 144 AA; 17270 MW; 00F1CFCD0007A09E CRC64;

  Query Match      64.1%; Score 25; DB 1; Length 144;
  Best Local Similarity 57.1%; Pred. No. 2.7e+02;
  Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
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Db 79 LDYDGD 85

RESULT 25
KLA2_ECOLI
ID KLA2_ECOLI STANDARD; PRT; 146 AA.
AC P52603; Q47333;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Antirestriction protein KicA.
GN KICA OR KILC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Larsen M.H., Figurski D.H.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
[2]
RC STRAIN=K12;
RX MEDLINE=95291464; PubMed=7773415;
RA Thomas C.W., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;
RT "Evolution of the kora-oriv segment of promiscuous IncP plasmids.";
RL Microbiology 141:1201-1210(1995).
CC -!- FUNCTION: COULD BE INVOLVED IN OVERCOMING RESTRICTION BARRIERS
CC DURING ESTABLISHMENT AFTER CONJUGATIVE TRANSFER.
CC -!- SIMILARITY: TO E.COLI YFUX.
CC -----
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CC -----
DR EMBL; U05773; AAA57448.1; -.
DR EMBL; L13392; AAA75284.1; -.
DR PIR; A55857; A55857.
DR PIR; I41323; I41323.
DR InterPro; IPR004914; Antirestrict.
DR Pfam; PF03230; Antirestrict; 1.
KW Plasmid.
FT CONFLICT 24 24 V -> VNF (IN REF. 2).
L -> P (IN REF. 2).
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FT CONFLICT 33 33 L -> P (IN REF. 2).
FT CONFLICT 77 77 R -> P (IN REF. 2).
SQ SEQUENCE 146 AA; 15867 MW; 9835588E26B8BA60 CRC64;

  Query Match      64.1%; Score 25; DB 1; Length 146;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDG 5
   :|::|:
Db 73 EHDG 76

RESULT 26
PPDD_ECOLI
ID PPDD_ECOLI STANDARD; PRT; 146 AA.
AC P36647; Q8RMZ6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prepilin peptidase dependent protein D precursor.
GN PPDD OR B0108.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=95047556; PubMed=7959070;
RA Whitchurch C.B., Mattick J.S.;
RT "Escherichia coli contains a set of genes homologous to those
RT involved in protein secretion, DNA uptake and the assembly of type-4
RT fimbriae in other bacteria.";
RL Gene 150:9-15(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94361430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[4]
RP PRELIMINARY SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Shatia R.S.;
RL Submitted (XXY-1993) to the EMBL/GenBank/DBJ databases.
[5]
RP IDENTIFICATION.
RA Rudd K.R.;
RL Unpublished observations (JAN-1994).
CC -!- FUNCTION: Not yet known.
CC -----
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CC -----
DR EMBL; U28105; AAC36923.1; -.
L -> P (IN REF. 2).
```



```
DR EMBL; D26562; BAB96678.1; ALT_INIT.
DR EMBL; AE000119; AAC73219.1; -.
DR EMBL; L20834; -. NOT_ANNOTATED_CDS.
DR PIR; D64733; D64733.
DR HSP; P02974; 2PIL.
DR EcoGene; EG12107; ppdD.
DR InterPro; IPR001082; Pili.
DR Pfam; PF00114; pilin; 1.
DR ProDom; PD008666; Pilin; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Methylation; Complete proteome.
FT PROPEP 1 6 BY SIMILARITY.
FT CHAIN 7 146 PREPILIN PEPTIDASE DEPENDENT PROTEIN D.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
FT CONFLICT 1 5 MDKOR -> DQQT (IN REF. 2).
SQ SEQUENCE 146 AA; 15622 MW; 7905D78A1E8B17A0 CRC64;

Query Match 64.1%; Score 25; DB 1; Length 146;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
||| |
Db 58 LEHGGLD 64

RESULT 27
YH05_VACCV STANDARD; PRT; 60 AA.
AC YH05_VACCV
ID P17356;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Hypothetical 5.7 kDa HindIII-C protein.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073756; PubMed=2849238;
RA Kotwal G.J., Moss B.;
RT "Analysis of a large cluster of nonessential genes deleted from a
vaccinia virus terminal transposition mutant.";
RL Virology 167:524-537(1988).
CC -----
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CC -----
DR EMBL; M22812; AAA69598.1; -.
DR PIR; G31829; WZVZA7.
KW Hypothetical protein; Early protein.
SQ SEQUENCE 60 AA; 5680 MW; B29BDE019384BEB CRC64;

Query Match 61.5%; Score 24; DB 1; Length 60;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HDGIN 7
||| |
Db 19 HDGSN 23

RESULT 28
YDIE_ECOLI STANDARD; PRT; 63 AA.
ID YDIE_ECOLI
AC P40721;
```

```
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydie.
GN YDIE OR B1705 OR Z2734 OR ECS2412.
OS Escherichia coli, and
OC Escherichia coli, O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91323737; PubMed=1677907;
RA Hudson G.S., Relloe P., Davidson B.E.;
RT "Two promoters control the aroH gene of Escherichia coli.";
RL Gene 102:87-91(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubraman S.,
RA Tagami H., Takada J., Takeuchi K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509552;
MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
CC -!- SIMILARITY: TO Y. ENTEROCOLITICA HEMP.
CC -----
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DR EMBL; M3266; -; NOT ANNOTATED CDS.
DR EMBL; AE000266; AAC74775.1; -;
DR EMBL; D90813; BAA15474.1; -;
DR EMBL; AE005394; AAG56692.1; -;
DR EMBL; AF002558; BAB35835.1; -;
DR PIR; A64929; A64929.
DR PIR; D90930; D90930.
DR PIR; H85778; H85778.
DR EcoGene; EG12391; ydiE.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 63 AA; 7117 MW; ALEA3DD6F1DC69A1 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 63;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
DB 42 IDHDG 46

RESULT 29
Y082_BACAN
ID Y082_BACAN STANDARD; PRT; 69 AA.
AC Q9RMV3.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein pX02-82.
GN PX02-82.
OS Bacillus anthracis.
OG Bacillus anthracis.
OG Plasmid pX02.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RA Okinaka R.T., Cloud K., Hampton O., Hill K.K., Keim P., Lamke G.,
RA Kmano S., Manter D., Martinez Y., Svensson R., Tatum L.R.,
RA Brown A.E., Jackson P.J.
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF188935; AAF13686.1; -;
DR KW Hypothetical protein; Plasmid.
SQ SEQUENCE 69 AA; 8041 MW; B69DECA31451EAF4 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 69;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY -1 LEHDGI 6
DB 50 VEHDGI 55

RESULT 30
LGEN_BOVIN
ID LGEN_BOVIN STANDARD; PRT; 73 AA.
AC P59761;

DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactogenin (EC 3.1.27.-) (Fragments).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX TISSUE=Milk;
RX MEDLINE=99417543; PubMed=10486275;
RA Ye X.Y., Cheng K.J., Ng T.B.;
RT "Isolation and characterization of angiogenin-1 and a novel protein
RT designated lactogenin from bovine milk."
RL Biochem. Biophys. Res. Commun. 263:187-191 (1999).
RN [2]
RP INHIBITION OF HIV-1 REVERSE TRANSCRIPTASE.
RX MEDLINE=2055576; PubMed=11105990;
RA Wang H., Ye X.Y., Ng T.B.;
RT "First demonstration of an inhibitory activity of milk proteins
RT against human immunodeficiency virus-1 reverse transcriptase and the
RT effect of succinylatation";
RL Life Sci. 67:2745-2752 (2000).
CC -1- FUNCTION: Secretory RNase specific towards pyrimidine bases, with
CC higher activity towards poly C than poly U. Inhibits cell-free
CC translation. Inhibits HIV-1 reverse transcriptase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Milk.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR InterPro; IPR001427; RNaseA.
DR PRODom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; PARTIAL.
KW Hydrolase; Nuclease; Endonuclease; Antiviral;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT UNSURE 36 OR R.
FT UNSURE 37 OR E.
FT UNSURE 38 OR Q.
FT UNSURE 39 OR C.
FT UNSURE 40 OR R.
FT UNSURE 41 OR N.
FT UNSURE 42 OR C.
FT UNSURE 43 OR N.
FT NON_CONS 57 58
FT NON_TER 73 73
SQ SEQUENCE 73 AA; 8669 MW; 28DA862F43A9710F CRC64;

Query Match 61.5%; Score 24; DB 1; Length 73;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 59 EHEGV 63

RESULT 31
Z123_HUMAN
ID Z123_HUMAN STANDARD; PRT; 74 AA.
AC F35273;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 123 (H2F-1) (Fragment).
GN ZNF123.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=9312208; PubMed=1339395;
RA Saleh M., Sellieri L., Little P.F., Evans G.A.;
RT isolation and expression of linked zinc finger gene clusters on
RT human chromosome 11q;
RL Genomics 14:970-978(1992).
CC -!- FUNCTION: May act as a transcription regulator in developmental
CC processes.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Liver.
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC
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DR EMBL; S52506; AAB24880.1; -.
DR PIR; A44366; A44366.
DR Genew; HGNC:12906; ZNF123.
DR MIM; 194630; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0008355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
KW Nuclear protein; Repeat.
FT NON TER 1 1
FT ZN FING 6 28 C2H2-TYPE.
FT ZN FING 34 60 C2H2-TYPE.
FT NON TER 74 74
SQ SEQUENCE 74 AA; 8382 MW; DF3BED9F83E86FD6 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 74;
Best Local Similarity 28.6%; Pred. No. 2.1e+02;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEHGDGIN 7
Db 22 IQEGVH 28

RESULT 32
RNPH PSEST
ID RNPH PSEST STANDARD; PRT; 86 AA.
AC P5711;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein rnfH.
GN RNPH.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=A15;
RA Desnouches N., Lin M., Elmerich C.;
RT "Organisation of nif genes in Pseudomonas stutzeri A15, a rice
RT endophyte".
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the UPF0125 (znhf) family.
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DR EMBL; AJ297529; CAC03730.1; -.
DR HAMAP; MF 00460; -; 1.
DR InterPro; IPR005346; UPF0125.
DR Pfam; PF03658; UPF0125; 1.
FT DOMAIN 79 86 POLY-ASP.
SQ SEQUENCE 86 AA; 9688 MW; E1E3D6BED15CCD2B CRC64;

Query Match 61.5%; Score 24; DB 1; Length 86;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEHDDGI 6
Db 30 IEHSGV 35

RESULT 33
RL25 HAEIN
ID RL25 HAEIN STANDARD; PRT; 95 AA.
AC P45281;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L25.
GN RPL25 OR RPL25 OR H11630.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierliavage A.R., Sult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glöckel A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: BINDS TO THE 5S RNA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the L25P family of ribosomal proteins.
CC
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DR EMBL; U32836; AAC23277.1; -.
DR PIR; E64133; E64133.
DR HSSP; P02426; 1DFU.
DR TIGR; H11630; -.
DR InterPro; IPR001021; Ribosomal_L25.
DR Pfam; PF01386; Ribosomal_L25p_1.
DR ProDom; PD012503; Ribosomal_L25; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 95 AA; 10652 MW; A6711F78691B2A57 CRC64;
Query Match 61.5%; Score 24; DB 1; Length 95;

Best Local Similarity 57.1%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 2;

QY 1 LEHGDGIN 7
Db 43 LNHDELN 49

RESULT 34
RS6_CLOAB STANDARD; PRT; 95 AA.
AC Q97CX2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3US ribosomal protein S6.
GN RPSF OR CAC3724.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Neelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Ratusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum";
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
similarity).
CC -!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
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CC -----
DR EMBL; AF007867; AAKB1644.1; -
DR PIR; A97357; A97357.
DR HAMAP; MF 00360; -; 1.
DR InterPro; IPR000529; Ribosomal_S6.
DR Pfam; PF01250; Ribosomal_S6; 1.
DR ProDom; PD003809; Ribosomal_S6; 1.
DR TIGRFAMs; TIGR00166; S6; 1.
DR PROSITE; PS01048; RIBOSOMAL_S6; FALSE NEG.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 95 AA; 10912 MW; 578189E9D89D9B08 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 95;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGDGIN 7
Db 14 LDEEGIN 20

RESULT 35
CMGC_BACLI STANDARD; PRT; 97 AA.
AC Q8VQ71;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CMG operon protein 3 homolog precursor (late competence protein
comGC).

COMGC.
GN Bacillus licheniformis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RX MEDLINE=22003725; PubMed=12007649;
RA Lapidus A., Galleron N., Andersen J.T., Joergensen P.L., Ehrlich S.D.,
Sorokin A.;
RA "Co-linear scaffold of the Bacillus licheniformis and Bacillus
RT subtilis genomes and its use to compare their competence genes.";
RL FEMS Microbiol. Lett. 209:23-30(2002).
CC -!- FUNCTION: Required for transformation and DNA binding (By
similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: The unprocessed form is an integral membrane
CC protein with its C-terminus outside the membrane. Upon cleavage,
CC it is translocated to the outer face of the membrane (By
similarity).
CC -!- SIMILARITY: Belongs to the comGC family.
CC -----
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CC -----
DR EMBL; AF459917; AAL67531.1; -
DR InterPro; IPR000983; Bac_GSPG.
DR InterPro; IPR001120; ProK_N_methyl_S.
DR PRINTS; PR00813; BCTERIALGSPG.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Competence; Transport; Methylation; Transmembrane.
FT PROPEP 1 5
FT CHAIN 6 97 COMG OPERON PROTEIN 3 HOMOLOG.
FT MOD RES 6 26 POTENTIAL.
FT TRANSMEM 6 6 METHYLATION (BY SIMILARITY).
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 97 AA; 10726 MW; E4B7B11257BFF3A7 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 97;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHGD 5
Db 57 MDHGD 61

RESULT 36
PYD_DICLA STANDARD; PRT; 99 AA.
AC Q9FT99;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peptide YY-like precursor (PY).
GN PY.
OS Dicertrarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicertrarchus.
OX NCBI_TaxID=13489;
RN [1]

SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=98292845; PubMed=9629200;
RA Cerda-Reverter J.M., Martinez Rodriguez G., Zanuy S., Carrillo M.,
RA Larhammar D.;

RT "Cloning of neuropeptide Y, peptide YY, and peptide Y from sea bass
(Dicentrarchus labrax), a marine teleost.";

RL Ann. N.Y. Acad. Sci. 839:493-495(1998).

CC -|- FUNCTION: Gastrointestinal hormone and neuropeptide.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- SIMILARITY: Belongs to the NPY family.

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CC -----

CC EMBL; AJ053379; CAB4933.1; -

CC HSP; P01303; IRON.

CC InterPro; IPR001955; Pancreatic_horm.

CC Pfam; PF00159; hormone3; 1.

CC PRINTS; PR00278; PANCHORMONE.

CC ProDom; PD001267; Pancreatic_horm; 1.

CC SMART; SM00309; PAH; 1.

CC PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.

CC PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.

CC Hormone; Cleavage on pair of basic residues; Amidation; Signal;

CC Neuropeptide.

CC SIGNAL 1 27 POTENTIAL.

CC CHAIN 28 63 PEPTIDE YY-LIKE.

CC PROPEP 65 99 C-TERMINAL EXTENSION.

CC MOD_RES 63 63 AMIDATION (G-64 PROVIDE AMIDE GROUP)

CC (POTENTIAL).

CC SEQUENCE 99 AA; 11065 MW; 6897DEBABD4E74FD CRC64;

CC SQ

Query Match

Best Local Similarity 61.5%; Score 24; DB 1; Length 99;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy

3 HDGIN 7

|||||

22 HSGIN 26

Db

RESULT 37

FER2_CAUCR

ID FER2_CAUCR

AC P37098;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ferredoxin, 2Fe-2S (FdII).

GN FDXB OR FDXP OR C3524.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Caulobacter.

OX NCBI_TaxID=155892;

RN [1]_TaxID=155892;

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.

RA Amemiya K.;

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=95270612; PubMed=7751304;

RX Wang S.P., Chen Y.P., Ely B.;

RA "A ferredoxin, designated FdxP, stimulates p-hydroxybenzoate

RT hydroxylase activity in Caulobacter crescentus.";

RL J. Bacteriol. 177:2908-2911(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

CC -|- COFACTOR: Binds 1 2Fe-2S cluster (BY similarity).

CC -|- SIMILARITY: Belongs to the adrenodoxin / putidaredoxin family.

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CC -----

CC EMBL; X51607; CAJ35950.1; -

CC PIR; AE006011; AAK25486.1; -

CC HSP; P00259; 1GPX.

CC TIGR; CG3524; -

CC InterPro; IPR001055; Adrenodoxin.

CC InterPro; IPR001041; Ferredoxin.

CC Pfam; PF00111; fer2; 1.

CC PRINTS; PR00355; ADRENODOXIN.

CC PROSITE; PS00814; ADX; 1.

CC Electron transport; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;

CC Complete proteome.

FT METAL 40 40 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 86 86 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 86 86 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

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FT METAL 86 86 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

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DR EMBL; X83708; CAA58681.1; -
 DR PIR; PC4228; PC4228; Hexapep transf.
 DR InterPro; IPR001451; Hexapep transf.
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES; 1.
 DR Peptideglycan synthesis; Cell wall; Transferase;
 KW Nucleotidyltransferase; Repeat.
 FT NON TER 1
 SQ SEQUENCE 116 AA; 12106 MW; D27706B9B8F7B362 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 116;
 Best Local Similarity 42.9%; Pred. No. 3.5e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
 Db 42 VNYDGVN 48
 : : : : :
 : : : : :

RESULT 39
 FOLD STROCO STANDARD; PRT; 119 AA.
 AC QXK8IO;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dihydropyrimidin aldolase (EC 4.1.2.25) (DHNA).
 GN FOLB OR SCO3400 OR SCE9.07.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).

CC -!- FUNCTION: Catalyzes the conversion of 7,8-dihydropyrimidin to 6-
 CC hydroxymethyl-7,8-dihydropyrimidin (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2-amino-4-hydroxy-6-(D-erythro-1,2,3-
 CC trihydroxypropyl)-7,8-dihydropteridine = 2-amino-4-hydroxy-6-
 CC hydroxymethyl-7,8-dihydropteridine + glycolaldehyde.
 CC -!- PATHWAY: Folate biosynthesis.
 CC -!- SIMILARITY: Belongs to the DHNA family.
 CC -----

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 CC -----

DR EMBL; AL939116; CAB42753.1; -
 DR PIR; T36326; T36326.
 DR HSRF; P56740; 1DHN.

DR InterPro; IPR006157; FOLB.
 DR InterPro; IPR006156; FOLB_fam.
 DR Pfam; PF02152; FOLB; 1.
 DR TIGRFAMs; TIGR00525; folB; 1.
 DR TIGRFAMs; TIGR00526; folB_dom; 1.
 KW Lyase; Folate biosynthesis; Complete proteome.
 SQ SEQUENCE 119 AA; 13002 MW; 0E86573FA1A694D CRC64;

Query Match 61.5%; Score 24; DB 1; Length 119;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDGI 6
 Db 84 LKHEGV 89
 : : : : :
 : : : : :

RESULT 40
 PHNA_HAEIN STANDARD; PRT; 120 AA.
 ID PHNA_HAEIN STANDARD; PRT; 120 AA.
 AC P44479;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE PhnA protein homolog.
 DE PHNA OR H10046.
 GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.D., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 CC -----

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DR EMBL; U32690; AAC21724.1; -
 DR PIR; I64044; I64044.
 DR TIGR; H10046; -
 DR InterPro; IPR004624; PhnA.
 DR Pfam; PF03831; PhnA; 1.
 DR TIGRFAMs; TIGR00696; phnA; 1.
 KW Complete proteome.
 SQ SEQUENCE 120 AA; 13678 MW; 5553FE2ACC6C6245 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 120;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HDGIN 7
 Db 29 HDSIN 33
 : : : : :
 : : : : :

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RESULT 41
YDEP_BACSU STANDARD; PRT; 128 AA.
ID YDEP_BACSU STANDARD; PRT; 128 AA.
AC P96573; C31495;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ydep.
GN YDEP OR BSU05290.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
RT Bacillus subtilis genome.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunze F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bortner M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrai E., Foulger D.,
RA Friiz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Goughly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koeter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
CC -!- SIMILARITY: Belongs to the UPF0087 family.
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CC EMBL; AB001488; BAA19363.1; ALT_INIT.
CC EMBL; Z99106; CAB12336.1; -.
CC PIR; B69779; B69779.
CC Subtilist; BG12143; ydep.
CC InterPro; IPR002577; DUF24.
CC Pfam; PF01638; DUF24; 1.
CC ProDom; PD004032; DUF24; 1.
CC Hypothetical protein; Complete proteome.
CC SEQUENCE 128 AA; 15211 MW; A47D416545CCA5C8 CRC64;
-----
Query Match 61.5%; Score 24; DB 1; Length 128;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEHDI 6
Db 68 LERDGV 73
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RESULT 42
MRKF_KLEPN STANDARD; PRT; 132 AA.
ID MRKF_KLEPN STANDARD; PRT; 132 AA.
AC P21650;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE MrKF protein.
GN MRKF.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IA565;
RX MEDLINE=91100388; PubMed=1670938;
RA Allen B.L., Gerlach G.-F., Clegg S.;
RA "Nucleotide sequence and functions of mrk determinants necessary for
RT expression of type 3 fimbriae in Klebsiella pneumoniae.";
RL J. Bacteriol. 173:916-920 (1991).
CC -!- FUNCTION: APPEARS TO AFFECT THE STABILITY OF THE INTACT FIMBRIAE
CC ON THE CELL SURFACE.
CC -!- SUBCELLULAR LOCATION: Fimbria.
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CC EMBL; M55912; AAA25097.1; -.
CC PIR; F39142; F39142.
CC InterPro; IPR008966; Adhes_bact.
CC Fimbria.
SQ SEQUENCE 132 AA; 14531 MW; 1C821B681912BC1A CRC64;
-----
Query Match 61.5%; Score 24; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEHDI 5
Db 15 LRHDG 19
-----
RESULT 43
RS12_ERYGR STANDARD; PRT; 132 AA.
ID RS12_ERYGR STANDARD; PRT; 132 AA.
AC OS9936;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S12.
GN RPS12 OR ERPR1.
OS Erysiphe graminis (subsp. hordei) (Grass mildew) (Blumeria graminis
OC (subsp. hordei)).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Erysiphales; Erysiphaceae; Blumeria.
OX NCBI_TaxID=62688;
RN [1]
```

RP SEQUENCE FROM N.A.
RA Zhang Z., Gurr S.J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 12-132 FROM N.A.
RA Zhang Z.G., Gurr S.J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the S12E family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AF052483; AAC15834.1; -;
CC EMBL; AF051259; AAC15802.1; -;
CC InterPro; IPR004038; Ribosomal L7A.
CC Pfam; PF01248; Ribosomal L7Ae; 1.
CC PRINTS; PR00972; RIBOSOMAL_S12E.
CC PROSITE; PS01189; RIBOSOMAL_S12E; 1.
KW Ribosomal protein.
SQ SEQUENCE 132 AA; 14632 MW; 91F3F48DA07917B4 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 132;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGI 6
DB 26 LMHDGL 31

RESULT 44
SPAK_SHIFL STANDARD; PRT; 133 AA.
AC P35530;
DT 01-JUN-1994 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Surface presentation of antigens protein spak (Spa15 protein).
GN SPAK OR SPA15 OR CP0148.
OS Shigella flexneri.
OG Plasmid pWR100, Plasmid pMYSH6000, and Plasmid pCP301.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=92193289; PubMed=1312536;
RA Venkatesan M.M., Buysse J.M., Oaks E.V.;
RT "Surface presentation of Shigella flexneri invasion plasmid antigens
RT requires the products of the spa locus."
RL J. Bacteriol. 174:1990-2001(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaser P., Rusniok C., Nedjari H., d'Hauteville H.,
RA Kunst F., Sansonetti P., Parsot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
RT by the type III secretion apparatus of Shigella flexneri";
RL Mol. Microbiol. 38:760-771(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=21189246; PubMed=11293750;
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
RA Blattner F.R.;

RT "Complete DNA sequence and analysis of the large virulence plasmid of
RT Shigella flexneri".
RL Infect. Immun. 69:3271-3285(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=YSH6000 / Serotype 2a; PLASMID=pMYSH6000;
RX MEDLINE=93224456; PubMed=8385666;
RA Sasaki K., Komatsu K., Tobe T., Suzuki T., Yoshikawa M.;
RT Eight genes in region 5 that form an operon are essential for
RT invasion of epithelial cells by Shigella flexneri 2a".
RL J. Bacteriol. 175:2334-2346(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a; PLASMID=pCP301;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding X., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -!- FUNCTION: REQUIRED FOR SURFACE PRESENTATION OF INVASION PLASMID
CC ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION
CC COMPETENCE OF THE IPA ANTIGENS.
CC -!- SIMILARITY: BELONGS TO THE SPAK FAMILY.
CC -----
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CC -----
CC EMBL; M81458; AAA26540.1; -;
CC EMBL; AL391753; CAC05823.1; -;
CC EMBL; AF348706; AAK18467.1; -;
CC EMBL; D13663; BAA02824.1; -;
CC EMBL; AF386526; AAL72308.1; -;
CC PIR; B42284; B42284.
CC InterPro; IPR003065; Invas Spak.
CC Pfam; PF03519; Invas Spak; 1.
CC PRINTS; PR01305; SSPAKPROTEIN.
CC ProDom; PD016047; Invas Spak; 1.
KW Plasmid; Virulence; Complete proteome.
SQ SEQUENCE 133 AA; 15116 MW; EA8F145A85A002B1 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGI 6
DB 110 HDGI 113

RESULT 45
SPAK_SHISO STANDARD; PRT; 133 AA.
AC Q55296;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Surface presentation of antigens protein spak (Spa15 protein).
GN SPAK OR SPA15.
OS Shigella sonnei.
OG Plasmid.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=624;
RN [1]

RP SEQUENCE FROM N.A.
RA Arakawa E., Kato J.I., Ito K.I., Watanabe H.;
RT "Comparison and high conservation of nucleotide sequences of spa-mxi
RI regions between S.sonnei and S.flexneri -- identification of a new
RI gene coding plausible membrane protein."
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR SURFACE PRESENTATION OF INVASION PLASMID
CC ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION
CC COMPETENCE OF THE IPA ANTIGENS.
CC -!- SIMILARITY: BELONGS TO THE SPAK FAMILY.
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CC -----
CC EMBL; D50601; BAA09157.1; -
DR InterPro; IPR003065; Invas_Spak.
DR Pfam; PF03519; Invas_Spak; 1.
DR PRINTS; PR01305; SSPAKPROTEIN.
DR ProDom; PD016047; Invas_Spak; 1.
KW Plasmid; Virulence.
SQ SEQUENCE 133 AA; 15188 MW; EA9F173A85A002B1 CRC64;

Query Match 61.5%; Score 24; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGI 6
Db 110 HDGI 113

Search completed: June 15, 2004, 12:23:19
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 12:22:52 ; Search time 40 Seconds
(without alignments)
55.216 Million cell updates/sec

Title: US-09-394-019c-212

Perfect score: 39

Sequence: 1 LEHGDIN 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 311989

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	32	82.1	128	Q9YAM4	Q9YAM4 aeropyrum p
2	31	79.5	67	Q8UIM7	Q8UIM7 pyrococcus
3	30	76.9	63	Q9ETE4	Q9ETE4 oryza sativ
4	30	76.9	64	Q8ET59	Q8ET59 mus musculu
5	30	76.9	78	Q8XSB6	Q8XSB6 raltstonia s
6	30	76.9	80	Q9KRZ6	Q9KRZ6 vibrio chol
7	30	76.9	80	Q8PBA1	Q8PBA1 xanthomonas
8	30	76.9	89	Q8UWJ1	Q8UWJ1 gallus gall
9	30	76.9	97	Q9L2K5	Q9L2K5 streptomyce
10	30	76.9	114	Q8DQK6	Q8DQK6 streptococc
11	30	76.9	122	Q9J5E5	Q9J5E5 fowlpox vir
12	30	76.9	136	Q8LQ98	Q8LQ98 oryza sativ
13	30	76.9	142	Q91BT7	Q91BT7 helicoverpa
14	30	76.9	144	Q9E215	Q9E215 helicoverpa
15	30	76.9	144	Q9IFI9	Q9IFI9 helicoverpa
16	30	76.9	146	Q8CWE3	Q8CWE3 escherichia

17	29	74.4	55	11	Q99JC7	Q99JC7 rattus norv
18	29	74.4	59	6	Q95KU8	Q95KU8 bos taurus
19	29	74.4	67	2	Q47667	Q47667 escherichia
20	29	74.4	68	13	Q42337	Q42337 xenopus lae
21	29	74.4	73	2	Q93877	Q93877 staphylococ
22	29	74.4	77	16	Q8KCM0	Q8KCM0 chlorobium
23	29	74.4	82	16	Q838W3	Q838W3 enterococcu
24	29	74.4	88	7	Q860C7	Q860C7 acrocephalu
25	29	74.4	88	7	Q860C6	Q860C6 acrocephalu
26	29	74.4	88	7	Q860C5	Q860C5 acrocephalu
27	29	74.4	88	7	Q860C4	Q860C4 acrocephalu
28	29	74.4	88	7	Q860C3	Q860C3 acrocephalu
29	29	74.4	90	7	Q860C9	Q860C9 acrocephalu
30	29	74.4	97	6	Q8SEJ5	Q8SEJ5 equus cabal
31	29	74.4	97	6	Q8SEJ5	Q8SEJ5 sus scrofa
32	29	74.4	98	6	Q9NIC0	Q9NIC0 ovis aries
33	29	74.4	100	4	Q9UMB0	Q9UMB0 homo sapien
34	29	74.4	109	16	Q8P1F8	Q8P1F8 xanthomonas
35	29	74.4	117	9	Q8W6N9	Q8W6N9 bacterioph
36	29	74.4	117	16	Q8FE20	Q8FE20 xanthomonas
37	29	74.4	124	2	Q8KSU0	Q8KSU0 rhizobium l
38	29	74.4	137	4	Q9HBN2	Q9HBN2 homo sapien
39	29	74.4	138	12	Q9DHI4	Q9DHI4 yaba-like d
40	29	74.4	141	5	Q9Y1T3	Q9Y1T3 jasus edwar
41	29	74.4	146	17	Q97XH7	Q97XH7 sulfolobus
42	29	74.4	146	17	Q972G0	Q972G0 sulfolobus
43	29	74.4	147	16	Q89FE7	Q89FE7 bradyrhizob
44	28	71.8	22	2	Q34195	Q34195 enrlichia r
45	28	71.8	69	16	Q81RR9	Q81RR9 bacillus an

ALIGNMENTS

RESULT 1

Q9YAM4
ID Q9YAM4 PRELIMINARY; PRT; 128 AA.
AC Q9YAM4: (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein APE1919.
GN APE1919.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcales; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabavasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RT DNA Res. 8:82-101(1999).
RL EMBL; AP000062; BAA80924.1; --
DR EMBL; G72579; G72579.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 128 AA; 13027 MW; 20FC54839DE21121 CRC64;

Query Match 82.1%; Score 32; DB 17; Length 128;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGDIN 7
Db 116 LSHDGLN 122

```

RESULT 2
Q8UIM7
ID Q8UIM7 PRELIMINARY; PRT; 67 AA.
AC Q8UIM7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein P11179.
GN P11179.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 9422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010226; AAL81303.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 67 AA; 7561 MW; 591FE1D4A09AF560 CRC64;

Query Match 75.5%; Score 31; DB 17; Length 67;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHGGI 6
Db 41 LEHGGI 46

RESULT 3
Q9FTE4
ID Q9FTE4 PRELIMINARY; PRT; 63 AA.
AC Q9FTE4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0698A04.7 protein (P0494A10.23 protein).
GN P0698A04.7 OR P0494A10.23.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatodeae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0698A04.7."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0494A10.23."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002868; BAB17146.1; -.
DR EMBL; AP002541; BAB55483.1; -.
DR Gramene; Q9FTE4; -.
SQ SEQUENCE 63 AA; 6601 MW; 294AC4BDEC79948D CRC64;

Query Match 76.9%; Score 30; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDGIN 7
Db 58 HDGIN 62

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RESULT 4
Q8BT59
ID Q8BT59 PRELIMINARY; PRT; 64 AA.
AC Q8BT59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junction cell adhesion molecule 3 (Fragment).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK017692; BAC25526.1; -.
FT NON TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 76.9%; Score 30; DB 11; Length 64;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHDGIN 7
Db 41 KHDGIN 46

RESULT 5
Q8XSB6
ID Q8XSB6 PRELIMINARY; PRT; 78 AA.
AC Q8XSB6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein RSP0562.
GN RSP0562 OR RS03916.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502 (2002).
DR EMBL; AL646079; CAD17113.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR002577; DUF24.
DR Pfam; PF01638; DUF24; 1.
DR ProDom; PD004032; DUF24; 1.
DR Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 78 AA; 8318 MW; 0AE00EAB5C9A3B0A CRC64;

Query Match 76.9%; Score 30; DB 16; Length 78;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LEHNGI 6
Db      56 LEHNGM 61

RESULT 6
ID Q9KRZ6 PRELIMINARY; PRT; 80 AA.
AC Q9KRZ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VC1487.
GN VC1487.cholerae.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unwayan L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Ueberback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AB004226; AAF94642.1; -.
DR PIR; H82194; H82194.
DR TIGR; VC1487; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 80 AA; 9275 MW; F6B667C37C4F6892 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 80;
Best Local Similarity 71.4%; Pred. No. 1.le+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEHNGIN 7
Db      71 LKHNGIN 77

RESULT 7
ID Q8PBA1 PRELIMINARY; PRT; 80 AA.
AC Q8PBA1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE HrpD6 protein.
GN HRPD6 OR XC1222.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=1202417;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AB012221; AAM40520.1; -.
KW Complete proteome.
SQ SEQUENCE 80 AA; 8787 MW; E723B262314DA11E CRC64;

Query Match 76.9%; Score 30; DB 16; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HDGIN 7
Db      63 HDGIN 67

RESULT 8
ID Q8UWJ1 PRELIMINARY; PRT; 89 AA.
AC Q8UWJ1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl-x (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432511; AAL35559.1; -.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10124 MW; B5B0EBE5F323A8C4 CRC64;

Query Match 76.9%; Score 30; DB 13; Length 89;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEHNGIN 7
Db      50 LFHDGIN 56

RESULT 9
ID Q9L2K5 PRELIMINARY; PRT; 97 AA.
AC Q9L2K5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO0699.

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SC00699 OR SCF42.09C.
 Streptomyces coelicolor.
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939106; CAB69671.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 97 AA; 10089 MW; 4CFD924E273194F5 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 97;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDSI 6
 |::|::|
 DB 35 LHDHGI 40

RESULT 10
 ID Q8DQ6 PRELIMINARY; PRT; 114 AA.
 AC Q8DQ6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE ABC transporter ATP-binding protein-glutamine, truncation.
 GN GLN-TRUNCATION OR SPR0535.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
 LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Niclas T.I.,
 Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rockey P.,
 Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
 Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 DR EMBL; AE008432; AAK93339.1; -.
 DR PIR; G97938; G97938.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 114 AA; 12665 MW; 32315A476EF6AD51 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 114;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDSI 7
 |::|::|
 DB 47 LAHDGMN 53

RESULT 11
 ID Q9J5B5 PRELIMINARY; PRT; 122 AA.
 AC Q9J5B5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF FPV066 hypothetical protein.
 GN FPV066.
 OS Fowlpox virus (FPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OX NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193820; PubMed=10729156;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RT "The genome of fowlpox virus.";
 RL J. Virol. 74:3815-3831(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF198100; AAF44410.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 122 AA; 14797 MW; 908629B0DB871662 CRC64;

Query Match 76.9%; Score 30; DB 12; Length 122;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDSI 7
 |::|::|
 DB 10 LKHDGIS 16

RESULT 12
 ID Q8LQ98 PRELIMINARY; PRT; 136 AA.
 AC Q8LQ98;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE B1011A07.14 protein.
 GN B1011A07.14.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
 clone:B1011A07.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003722; BAB92766.1; -.
 DR Gramene; Q8LQ98; -.
 SQ SEQUENCE 136 AA; 14422 MW; 07F19447102FD19D CRC64;

Query Match 76.9%; Score 30; DB 10; Length 136;
 Best Local Similarity 57.1%; Pred. No. 2e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
DB 121 VSHDGVN 127

RESULT 13

Q91BT7 PRELIMINARY; PRT; 142 AA.
AC Q91BT7 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Helicoverpa armigera nuclear polyhedrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=51313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1;
RX PubMed=12050807;
RA Zhang C.X., Wu J.C.;
RT "Genome structure and the p10 gene of the Helicoverpa armigera nucleopolyhedrovirus.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C1;
RA Zhang C.X., Jin W.R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF303045; AAK96369.1; -;
KW Hypothetical protein.
SQ SEQUENCE 142 AA; 16036 MW; 45D3B56DAE934C82 CRC64;

Query Match 76.9%; Score 30; DB 12; Length 142;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

QY 3 HDGIN 7
DB 60 HDGIN 64

RESULT 14

Q9E215 PRELIMINARY; PRT; 144 AA.
AC Q9E215 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Orf435-like protein (ORF129).
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RC Robertson A.P.S.;
RA "Genetic organization of Helicoverpa zea nuclear polyhedrosis virus in the region of EcoRI U,D,L,A and Q.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
RA Fresnail J.K., Herrmann R., Dotan M., Tingey S., Hu Z.-H., Vlask J.M.;
RT "Genome sequence analysis of Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275264; AAG17387.1; -;
DR EMBL; AF334030; AAL56135.1; -;
SQ SEQUENCE 144 AA; 16214 MW; A38170147F20782A CRC64;

Query Match 76.9%; Score 30; DB 12; Length 144;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;

QY 3 HDGIN 7
DB 60 HDGIN 64

RESULT 15

Q91FI9 PRELIMINARY; PRT; 144 AA.
AC Q91FI9 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF435 (Hypothetical protein).
OS Helicoverpa armigera nuclear polyhedrosis virus, and
OS Helicoverpa armigera nucleopolyhedrovirus G4.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=51313, 148363;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus;
RX MEDLINE=20033815; PubMed=10584750;
RA Chen X., Ijkel W.F., Dominy C., de Andrade Zanotto P.M., Hashimoto Y.,
RA Faktor O., Hayakawa T., Wang C.H., Prekumar A., Mathavan S.,
RA Krell P.J., Hu Z., Vlask J.M.;
RT "Identification, sequence analysis and phylogeny of the lef-2 gene of Helicoverpa armigera single-nucleocapsid baculovirus.";
RL Virus Res. 65:21-32(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus;
RA Long G., Chen X., Vlask J.M., Hu Z.;
RT "Genetic organization of the HindIII-I region of Helicoverpa armigera single-nucleocapsid nucleopolyhedrovirus.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RA Deng F., Chen X., Vlask J.M., Arif B.M., Hu Z.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bingdaxue 15:35-42(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RA Wang H., Hu Z., Sun X., Vlask J.M., Chen X.;
RT "Sequence analysis of the iap3 gene of Heliothis armigera single-nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bingdaxue 15:43-49(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RX MEDLINE=21078302; PubMed=11210934;
RA Wang H., Chen X., Wang H., Arif B.M., Vlask J.M., Hu Z.;
RT "Nucleotide sequence and transcriptional analysis of a putative basic DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
RL Virus Genes 22:113-120(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RX PubMed=11125177;
RA Chen X., Ijkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
RA Peters S., Zuidema D., Lankhorst R.K., Vlask J.M., Hu Z.;
RT "The sequence of the Helicoverpa armigera single-nucleocapsid nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 82:241-257(2001).
RN [7]
RP SEQUENCE FROM N.A.

RC SPECIES=Helicoverpa armigera nucleopolydnavirus G4;
RA Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.,
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF266697; AAF78940.1; -;
DR EMBL; AF271059; AAG53868.1; -;
KW Hypothetical protein.
SQ SEQUENCE 144 AA; 16115 MW; A3816C6476506D2A CRC64;

Query Match 76.9%; Score 30; DB 12; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
Db 60 HDGIN 64

RESULT 16
Q8CWE3 PRELIMINARY; PRT; 146 AA.
ID Q8CWE3
AC Q8CWE3
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Prepilin peptidase dependent protein D precursor.
GN PPDB OR C0127.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINS=O6:H1 / CPT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA McInley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016755; AAN78625.1; -;
DR GO; GO:0009289; C:filmbria; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001082; Pili.
DR InterPro; IPR001120; Prok_N_methyl_S.
DR Pfam; PF00114; Pili; 1.
DR ProDom; PD000666; Pili; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Complete proteome.
SQ SEQUENCE 146 AA; 15608 MW; 2305DABEA13F6ADCD CRC64;

Query Match 76.9%; Score 30; DB 16; Length 146;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGIN 7
Db 58 LEHGIN 64

RESULT 17
Q99UC7 PRELIMINARY; PRT; 55 AA.
ID Q99UC7
AC Q99UC7
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Soluble fibroblast growth factor receptor IIIB (Fragment).
GN SKGF-R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Testis;
RA Konrad L.;
RT "Expression of soluble FGF-R IIIB in testicular cell lines."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ312745; CAC37408.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
KW Receptor.
FT NON_TER
SQ SEQUENCE 55 AA; 6083 MW; 69886E17147DC94E CRC64;

Query Match 74.4%; Score 29; DB 11; Length 55;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGIN 7
Db 1 LKHGIN 7

RESULT 18
Q95KU8 PRELIMINARY; PRT; 59 AA.
ID Q95KU8
AC Q95KU8
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 2 (Fragment).
GN FGFR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Berisha B.A., Schams D.;
RT "Expression of fibroblast growth factor family in the bovine placenta
during the pregnancy";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ419173; CAD11602.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 59 AA; 6355 MW; 263284C9F573D36B CRC64;

Query Match 74.4%; Score 29; DB 6; Length 59;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHGIN 7
Db 49 LKHGIN 55

RESULT 19
Q47667 PRELIMINARY; PRT; 67 AA.
ID Q47667
AC Q47667
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Coli Su+6 (supp) amber suppressor transfer RNA-Leu.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85009179; PubMed=6207302;
RA Yoshimura M., Inokuchi H., Ozeki H.;
RT "Identification of Transfer RNA Suppressors in Escherichia coli.";
RL J. Mol. Biol. 177:627-644(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8811893; PubMed=2448476;
RA Nomura T., Fujita N., Ishihama A.;
RT "Expression of the leuX gene in Escherichia coli: regulation at
RT transcription and tRNA processing steps.";
RL J. Mol. Biol. 197:659-670(1987).
DR EMBL; X04174; CAA2774.1; -.
SQ SEQUENCE 67 AA; 7308 MW; 57BBF7985FF94A31 CRC64;

Query Match 74.4%; Score 29; DB 2; Length 67;
Best Local Similarity 83.3%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 2 EHDGIN 7
Db 48 EYDGIN 53

RESULT 20
O42337 PRELIMINARY; PRT; 68 AA.
ID O42337
AC O42337;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 2b (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiozaki C., Asano-Miyoshi M., Tashiro K., Shiokawa K., Emori Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D31760; BAA22058.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR007110; IG-like.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 68 68
SQ SEQUENCE 68 AA; 7561 MW; F4AE6489E37B1F07 CRC64;

Query Match 74.4%; Score 29; DB 13; Length 68;
Best Local Similarity 71.4%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

QY 1 LEHDGIN 7
Db 6 LEHSGIN 12

RESULT 21
Q936F7 PRELIMINARY; PRT; 73 AA.
ID Q936F7
AC Q936F7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
```

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RC STRAIN=M;
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RT "The Typhoid Capsular Polysaccharide of Staphylococcus aureus is carried
RT in a Staphylococcal Cassette Chromosome Genetic Element.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10927; AL26681.1; -.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8313 MW; 11766B088F91B37C CRC64;

Query Match 74.4%; Score 29; DB 2; Length 73;
Best Local Similarity 71.4%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

QY 1 LEHDGIN 7
Db 50 LEHEAIN 56

RESULT 22
Q8KCM0 PRELIMINARY; PRT; 77 AA.
ID Q8KCM0
AC Q8KCM0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein CT1395.
GN CT1395.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobiaceae.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=2210368; PubMed=1203901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Eison R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012897; AAM72623.1; -.
DR TIGR; CT1395; -.
KW Hypothetical protein; Complete proteome
SQ SEQUENCE 77 AA; 8578 MW; C9BA18618BEC1356 CRC64;

Query Match 74.4%; Score 29; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 LEHDG 5
Db 62 LEHDG 66

RESULT 23
Q838W3 PRELIMINARY; PRT; 82 AA.
ID Q838W3
AC Q838W3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN EF0320.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seehadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac J., Beanan M., Nelson W.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Khouri H.,
RA Yamathavan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AF016947; AA080183.1; -.
DR TIGR; EF0320; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 82 AA; 9049 MW; BECF70F37AB46120 CRC64;

Query Match 74.4%; Score 29; DB 16; Length 82;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EHDGIN 7
DB 24 EHSGIN 29

RESULT 24
Q860C7 PRELIMINARY; PRT; 88 AA.
AC Q860C7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdaal H., Wittzell H., von Schantz T.;
RT DGGE;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49697; AAP37625.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10095 MW; B7AFE336C0205727 CRC64;

Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 56 EHDGI 60

RESULT 25
Q860C6 PRELIMINARY; PRT; 88 AA.
AC Q860C6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdaal H., Wittzell H., von Schantz T.;
RT DGGE;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49697; AAP37625.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10095 MW; B7AFE336C0205727 CRC64;

Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 56 EHDGI 60

RESULT 26
Q860C5 PRELIMINARY; PRT; 88 AA.
AC Q860C5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdaal H., Wittzell H., von Schantz T.;
RT DGGE;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49697; AAP37627.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10095 MW; B7AFE336C0205727 CRC64;

Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 56 EHDGI 60

RESULT 27
Q860C4 PRELIMINARY; PRT; 88 AA.
AC Q860C4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]

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OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdaal H., Wittzell H., von Schantz T.;
RT DGGE;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49698; AAP37626.1; -.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10101 MW; B575FB54E1C05723 CRC64;

Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 56 EHDGI 60

RESULT 26
Q860C5 PRELIMINARY; PRT; 88 AA.
AC Q860C5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdaal H., Wittzell H., von Schantz T.;
RT DGGE;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49699; AAP37627.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10095 MW; B7AFE336C0205727 CRC64;

Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
DB 56 EHDGI 60

RESULT 27
Q860C4 PRELIMINARY; PRT; 88 AA.
AC Q860C4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]

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RP SEQUENCE FROM N.A.
RA Westerdahl H., Wittzell H., von Schantz T.;
RT "MHC class I typing of great reed warblers by motif-specific PCR and
RT DGGE";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF449701; AAP37628.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10095 MW; B7AFE336C0205727 CRC64;
Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGI 6
Db 56 EHDGI 60
RESULT 28
Q860C3 PRELIMINARY; PRT; 88 AA.
AC Q860C3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;
RN [1]
RP SEQUENCE FROM N.A.
RA Westerdahl H., Wittzell H., von Schantz T.;
RT "MHC class I typing of great reed warblers by motif-specific PCR and
RT DGGE";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF449701; AAP37629.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10094 MW; BDAF4336C0205727 CRC64;
Query Match 74.4%; Score 29; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGI 6
Db 56 EHDGI 60
RESULT 29
Q860C9 PRELIMINARY; PRT; 90 AA.
AC Q860C9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN ACAR-UA.
OS Acrocephalus arundinaceus (great reed warbler).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.
OX NCBI_TaxID=39621;

[1]
RP SEQUENCE FROM N.A.
RA Westerdahl H., Wittzell H., von Schantz T.;
RT "MHC class I typing of great reed warblers by motif-specific PCR and
RT DGGE";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF449695; AAP37623.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10644 MW; 7B9E4EF186F5E9D4 CRC64;
Query Match 74.4%; Score 29; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHDGI 6
Db 56 EHDGI 60
RESULT 30
Q8SPLO PRELIMINARY; PRT; 97 AA.
AC Q8SPLO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF-7 receptor 2111b (Fragment).
GN FGFR2111B.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Endometrium;
RA Welter H., Bollwein H., Einspanier R.;
RT "Expression of horse endometrium";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439892; CAD29183.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR Receptor.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10666 MW; 02C276B3248B7F91 CRC64;
Query Match 74.4%; Score 29; DB 6; Length 97;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEHDGIN 7
Db 79 LKHGIN 85
RESULT 31
Q8SPJ5 PRELIMINARY; PRT; 97 AA.
AC Q8SPJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF-7 receptor 2111b (Fragment).
GN FGFR72111B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RA "FGS-system in porcine endometrium.";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439895; CAD29186.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
KW Receptor.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10666 MW; 02C276B3248B7F91 CRC64;

Query Match 74.4%; Score 29; DB 6; Length 97;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
DB 79 LKHSGIN 85

RESULT 32
Q9NICO PRELIMINARY; PRT; 98 AA.
AC Q9NICO;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 2 IIb (Fragment).
GN FGFR2IIb.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RA Chen C., Spencer T.E., Bazer F.W.;
RT "Fibroblast growth factor-10: A stromal mediator of epithelial
function in the ovine uterus.";
RL Biol. Reprod. 63:959-966(2000).
DR EMBL; AF213380; AAP26719.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
KW Receptor.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 10767 MW; B372C276B3248B7F CRC64;

Query Match 74.4%; Score 29; DB 6; Length 98;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
DB 79 LKHSGIN 85

RESULT 33
Q9UMB0 PRELIMINARY; PRT; 100 AA.
AC Q9UMB0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor receptor-related protein (Fragment).
GN X-SAM.
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91296403; PubMed=1648704;
RA Champion-Arnaud P., Ronsin C., Gilbert E., Gesnel M.C., Housaint E.,
RA Breathnach R.;
RT "Multiple mRNAs code for proteins related to the BSK fibroblast growth
factor receptor.";
RL Oncogene 6:979-987(1991).
DR EMBL; S40853; AAB19319.1; -.
DR EMBL; S40851; AAB19319.1; JOINED.
DR FIR; A41794; A41794.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; igf_1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 100 AA; 10847 MW; E92E028C34733E34 CRC64;

Query Match 74.4%; Score 29; DB 4; Length 100;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEHDGIN 7
DB 50 LKHSGIN 56

RESULT 34
Q8PIF8 PRELIMINARY; PRT; 109 AA.
AC Q8PIF8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Benzene 1,2-dioxygenase ferredoxin protein.
DR BEDB OR XAC2940.
GN Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., L.P.,
RA Cicarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.F., Lemos E.G.M., Lemos M.V.F.,
RA Locati B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.N., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities."
RL Nature 417:455-463(2002).
DR EMBL; AEC01936; AAM37785.1; -.
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR005806; Rieske_dom.
```

DR Pfam: PF00355; Rieske; 1.
 KW Dioxigenase; Complete proteome.
 SQ SEQUENCE 109 AA; 12250 MW; 04024C66C2B35EA23 CRC64;
 Query Match 74.4%; Score 29; DB 16; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGI 6
 DB 99 EHDGI 103
 RESULT 35
 Q8W6N9 PRELIMINARY; PRT; 117 AA.
 AC Q8W6N9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Gp61.
 GN 61.
 OS Bacteriophage phiE125.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 OC NCBI_TaxID=180504;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Woods D.E., Jeddeloh J.A., Fritz D.F., DeShazer D.;
 RT "Burkholderia thailandensis E125 Harbors a Temperate Bacteriophage
 Specific for Burkholderia mallei";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF447491; AAL40335.1; -
 SQ SEQUENCE 117 AA; 13882 MW; BF8C2A4B3B1DB2BE CRC64;
 Query Match 74.4%; Score 29; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EHDGI 6
 DB 14 EHDGI 18
 RESULT 36
 Q8PE20 PRELIMINARY; PRT; 117 AA.
 AC Q8PE20;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein XCC0163.
 GN XCC0163.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OC NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=ATCC 33913 / NCPPB 528;
 RC MEDLINE=22022145; PubMed=12024217;
 RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities";
 RL Nature 417:459-463 (2002).
 DR EMBL; AE012112; AM39482.1; -
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR PROSITE; PS00018; EF_HAND; 3.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 117 AA; 12918 MW; DE9063AC8DF999B6 CRC64;
 Query Match 74.4%; Score 29; DB 16; Length 117;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEHDGI 6
 DB 64 LDHGV 69
 RESULT 37
 Q8KSU0 PRELIMINARY; PRT; 124 AA.
 AC Q8KSU0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OC NCBI_TaxID=367;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22151066; PubMed=12019272;
 RX Basu S.S., Karbarz M.J., Raetz C.R.H.;
 RT "Expression Cloning and Characterization of the C28 Acyltransferase of
 Lipid A Biosynthesis in Rhizobium leguminosarum";
 RL J. Biol. Chem. 277:28959-28971 (2002).
 DR EMBL; AF510733; AAM4295.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 124 AA; 13113 MW; 390E5F95F3CFB5E5 CRC64;
 Query Match 74.4%; Score 29; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEHDG 5
 DB 98 LEHDG 102
 RESULT 38
 Q9HBN2 PRELIMINARY; PRT; 137 AA.
 AC Q9HBN2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human cDNA clones with function of inhibiting cancer cell

RT growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218028; AAG17270.1; -.
KW Hypothetical protein.
SQ SEQUENCE 137 AA; 15826 MW; 908666F1966195687 CRC64;

Query Match 74.4%; Score 29; DB 4; Length 137;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHGDIN 7
|:|:|:
Db 109 LQHGVN 115

RESULT 39

QSDH14
ID Q9DH14 PRELIMINARY; PRT; 138 AA.
AC Q9DH14;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 129R protein.
GN 129R.
OS Yaba-like disease virus (YLDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OX NCBI_TaxID=132475;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176366; PubMed=11277691;
RA Lee H.J., Essani K., Smith G.L.;
RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
RL Virology 281:170-192(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Lee H.J.;
RL Thesis (2000), Sir William Dunn School of Pathology, University of.
DR EMBL; AJ293568; CAC21367.1; -.
SQ SEQUENCE 138 AA; 16059 MW; 100FA621BDAB4108 CRC64;

Query Match 74.4%; Score 29; DB 12; Length 138;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEHGDIN 7
|:|:|:
Db 3 LEHDIIN 9

RESULT 40

Q9Y1T3
ID Q9Y1T3 PRELIMINARY; PRT; 141 AA.
AC Q9Y1T3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Metallothionein-like protein (Fragment).
GN Jasus edwardsii (red rock lobster).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Jasus.
OX NCBI_TaxID=95461;
RN [1]
RP SEQUENCE FROM N.A.
RA Khoo J.G.I., Sin F.Y.T.;
RT "Novel peptide gene sequence from the lobster Jasus edwardsii.";
RL Zool. Stud. 38:95-109(1999).
DR EMBL; AF091369; AAD37832.1; -.

FT NON TER 1 1
SQ SEQUENCE 141 AA; 14893 MW; 09551B769BB01430 CRC64;
Query Match 74.4%; Score 29; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDG 5
|:|:|:
Db 36 LEHDG 40

RESULT 41

Q97XH7
ID Q97XH7 PRELIMINARY; PRT; 146 AA.
AC Q97XH7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SSO1764.
GN SSO1764.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=1142726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sersen C.W., Van der Coost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
EL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AS006787; AAK41957.1; -.
DR PIR; F90337; F90337.
DR InterPro; IPR005544; HHE.
DR Pfam; PF03794; HHE; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 146 AA; 17058 MW; 039AA714C98B5E8D CRC64;

Query Match 74.4%; Score 29; DB 17; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEHDG 5
|:|:|:
Db 101 LEHDG 105

RESULT 42

Q972G0
ID Q972G0 PRELIMINARY; PRT; 146 AA.
AC Q972G0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein St1173.
GN St1173.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Nakamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, *Sulfolobus tokodaii* strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AF000985; BAB6208.1; -;
 DR InterPro; IPR005544; HHE.
 DR Pfam; PF03794; HHE; 2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 146 AA; 17266 MW; EA2A859AF0485D94 CRC64;

Query Match 74.4%; Score 29; DB 17; Length 146;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEHDG 5
 |||||
 DB 101 LEHDG 105

RESULT 43

Q89FE7 Q89FE7 PRELIMINARY; PRT; 147 AA.
 AC Q89FE7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE BL-6763 protein.
 GN BLR6763.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:193-197(2002).
 DR EMBL; AF005959; BAC52018.1; -;
 KW Complete proteome.
 SQ SEQUENCE 147 AA; 15940 MW; 68C38FE059012BB CRC64;

Query Match 74.4%; Score 29; DB 16; Length 147;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
 |||||
 DB 66 EHDGI 70

RESULT 44

C34195 C34195 PRELIMINARY; PRT; 22 AA.
 AC C34195;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE GROES (Fragment).
 GN GROES.
 OS Ehrlichia risticii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Neorickettsia.
 OX NCBI_TaxID=950;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97373904; PubMed=9230387;
 RA Sumner J.W., Nicholson W.L., Maessung R.F.;
 RT "PCR amplification and comparison of nucleotide sequences from the
 RT groESL heat shock operon of *Ehrlichia species*.";
 RL J. Clin. Microbiol. 35:2087-2092(1997).
 DR EMBL; U96732; AAB65632.1; -;
 DR InterPro; IPR001476; Chaprinin_Opn10.
 DR Pfam; PF00166; cpn10; 1.
 FT NON TER 1
 SQ SEQUENCE 22 AA; 2504 MW; 21D959D75191F620 CRC64;

Query Match 71.8%; Score 28; DB 2; Length 22;
 Best Local Similarity 80.0%; Pred. No. 70;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHDGI 6
 |||||
 DB 1 EHDGV 5

RESULT 45

Q81RR9 Q81RR9 PRELIMINARY; PRT; 69 AA.
 AC Q81RR9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN BA1971.
 OS *Bacillus anthracis* (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tectelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benson J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
 RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
 RA Fraser C.M.;
 RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 DR EMBL; AB017030; AAP25863.1; -;
 DR TIGR; BA1971; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 69 AA; 7803 MW; 687CA89236197C9 CRC64;

Query Match 71.8%; Score 28; DB 16; Length 69;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDGIN 7
 |||||
 DB 27 HDGLN 31

Search completed: June 15, 2004, 12:24:12
 Job time : 41 secs